

[illegible]

for Manno

c 375	13.8	14.8	45	15	AA056018	Human gene fibronin	c 448	13.6	14.6	41	24	AA08885	Protein 2 of the Num
c 376	13.8	14.8	46	22	AA052419	Pichia methanolica	c 449	13.6	14.6	41	24	AA08955	Human 2-hydroxy ac
c 377	13.8	14.8	45	22	AA06385	Human fibronogen b	c 450	13.6	14.6	41	24	AA09705	Human 2-hydroxy ac
c 378	13.8	14.8	46	15	AA015841	Antisense PCR prim	c 451	13.6	14.6	41	24	AA03486	Human hsp70
c 379	13.8	14.8	46	15	AA015841	Antisense PCR prim	c 452	13.6	14.6	42	20	AA03486	Human hsp70
c 380	13.8	14.8	46	20	AA01135	Test sequence from	c 453	13.6	14.6	42	20	AA01776	Test sequence from
c 381	13.8	14.8	46	22	AA03952	Human SNP flanking	c 454	13.6	14.6	42	24	AA01780	Murine TNF- α gene
c 382	13.8	14.8	47	14	AA03905	PCR primer 455 use	c 455	13.6	14.6	42	24	AA03467	Human hsp70
c 383	13.8	14.8	47	14	AA03905	PCR primer 455 use	c 456	13.6	14.6	42	24	AA03467	Human hsp70
c 384	13.8	14.8	47	14	AA03905	PCR primer 455 use	c 457	13.6	14.6	43	18	AA01721	Human hsp70
c 385	13.8	14.8	47	14	AA03905	PCR primer 455 use	c 458	13.6	14.6	43	18	AA01721	Human hsp70
c 386	13.8	14.8	47	14	AA03905	PCR primer 455 use	c 459	13.6	14.6	43	18	AA01721	Human hsp70
c 387	13.8	14.8	47	21	AA06232	Human map-related	c 460	13.6	14.6	43	18	AA06232	Human map-related
c 388	13.8	14.8	47	21	AA06232	Human map-related	c 461	13.6	14.6	43	18	AA06232	Human map-related
c 389	13.8	14.8	47	21	AA06232	Human map-related	c 462	13.6	14.6	43	18	AA06232	Human map-related
c 390	13.8	14.8	48	24	AA06724	Human secreted pro	c 463	13.6	14.6	43	18	AA06724	Human secreted pro
c 391	13.8	14.8	48	24	AA06724	Human secreted pro	c 464	13.6	14.6	43	18	AA06724	Human secreted pro
c 392	13.8	14.8	48	24	AA06724	Human secreted pro	c 465	13.6	14.6	43	18	AA06724	Human secreted pro
c 393	13.8	14.8	50	9	AA01884	Protein (c) for the	c 466	13.6	14.6	46	21	AA01884	Protein (c) for the
c 394	13.8	14.8	50	9	AA01884	Protein (c) for the	c 467	13.6	14.6	46	21	AA01884	Protein (c) for the
c 395	13.8	14.8	50	9	AA01884	Protein (c) for the	c 468	13.6	14.6	46	21	AA01884	Protein (c) for the
c 396	13.8	14.8	50	22	AA02897	Human SNP oligonuc	c 469	13.6	14.6	46	21	AA02897	Human SNP oligonuc
c 397	13.8	14.8	50	22	AA02897	Human SNP oligonuc	c 470	13.6	14.6	46	21	AA02897	Human SNP oligonuc
c 398	13.8	14.8	50	22	AA02897	Human SNP oligonuc	c 471	13.6	14.6	46	21	AA02897	Human SNP oligonuc
c 399	13.8	14.8	50	22	AA02897	Human SNP oligonuc	c 472	13.6	14.6	46	21	AA02897	Human SNP oligonuc
c 400	13.8	14.8	50	22	AA02897	Human SNP oligonuc	c 473	13.6	14.6	46	21	AA02897	Human SNP oligonuc
c 401	13.6	14.6	20	20	AA01894	PCR primer used to	c 474	13.6	14.6	46	22	AA01894	PCR primer used to
c 402	13.6	14.6	20	20	AA01894	PCR primer used to	c 475	13.6	14.6	46	22	AA01894	PCR primer used to
c 403	13.6	14.6	20	20	AA01894	PCR primer used to	c 476	13.6	14.6	46	22	AA01894	PCR primer used to
c 404	13.6	14.6	20	20	AA01894	PCR primer used to	c 477	13.6	14.6	46	22	AA01894	PCR primer used to
c 405	13.6	14.6	20	20	AA01894	PCR primer used to	c 478	13.6	14.6	46	22	AA01894	PCR primer used to
c 406	13.6	14.6	20	20	AA01894	PCR primer used to	c 479	13.6	14.6	46	22	AA01894	PCR primer used to
c 407	13.6	14.6	21	22	AA08373	Oligonucleotide A1	c 480	13.6	14.6	46	22	AA08373	Oligonucleotide A1
c 408	13.6	14.6	21	22	AA08373	Oligonucleotide A1	c 481	13.6	14.6	46	22	AA08373	Oligonucleotide A1
c 409	13.6	14.6	21	22	AA08373	Oligonucleotide A1	c 482	13.6	14.6	46	22	AA08373	Oligonucleotide A1
c 410	13.6	14.6	27	22	AA03904	Test TMC-coa redu	c 483	13.6	14.6	46	22	AA03904	Test TMC-coa redu
c 411	13.6	14.6	28	19	AA01165	Human secreted pro	c 484	13.6	14.6	46	22	AA01165	Human secreted pro
c 412	13.6	14.6	28	19	AA01165	Human secreted pro	c 485	13.6	14.6	46	22	AA01165	Human secreted pro
c 413	13.6	14.6	28	19	AA01165	Human secreted pro	c 486	13.6	14.6	46	22	AA01165	Human secreted pro
c 414	13.6	14.6	28	19	AA01165	Human secreted pro	c 487	13.6	14.6	46	22	AA01165	Human secreted pro
c 415	13.6	14.6	28	19	AA01165	Human secreted pro	c 488	13.6	14.6	46	22	AA01165	Human secreted pro
c 416	13.6	14.6	28	19	AA01165	Human secreted pro	c 489	13.6	14.6	46	22	AA01165	Human secreted pro
c 417	13.6	14.6	28	19	AA01165	Human secreted pro	c 490	13.6	14.6	46	22	AA01165	Human secreted pro
c 418	13.6	14.6	28	19	AA01165	Human secreted pro	c 491	13.6	14.6	46	22	AA01165	Human secreted pro
c 419	13.6	14.6	28	19	AA01165	Human secreted pro	c 492	13.6	14.6	46	22	AA01165	Human secreted pro
c 420	13.6	14.6	28	19	AA01165	Human secreted pro	c 493	13.6	14.6	46	22	AA01165	Human secreted pro
c 421	13.6	14.6	28	19	AA01165	Human secreted pro	c 494	13.6	14.6	46	22	AA01165	Human secreted pro
c 422	13.6	14.6	28	19	AA01165	Human secreted pro	c 495	13.6	14.6	46	22	AA01165	Human secreted pro
c 423	13.6	14.6	28	19	AA01165	Human secreted pro	c 496	13.6	14.6	46	22	AA01165	Human secreted pro
c 424	13.6	14.6	28	19	AA01165	Human secreted pro	c 497	13.6	14.6	46	22	AA01165	Human secreted pro
c 425	13.6	14.6	28	19	AA01165	Human secreted pro	c 498	13.6	14.6	46	22	AA01165	Human secreted pro
c 426	13.6	14.6	28	19	AA01165	Human secreted pro	c 499	13.6	14.6	46	22	AA01165	Human secreted pro
c 427	13.6	14.6	28	19	AA01165	Human secreted pro	c 500	13.6	14.6	46	22	AA01165	Human secreted pro
c 428	13.6	14.6	28	19	AA01165	Human secreted pro	c 501	13.6	14.6	46	22	AA01165	Human secreted pro
c 429	13.6	14.6	28	19	AA01165	Human secreted pro	c 502	13.6	14.6	46	22	AA01165	Human secreted pro
c 430	13.6	14.6	28	19	AA01165	Human secreted pro	c 503	13.6	14.6	46	22	AA01165	Human secreted pro
c 431	13.6	14.6	28	19	AA01165	Human secreted pro	c 504	13.6	14.6	46	22	AA01165	Human secreted pro
c 432	13.6	14.6	28	19	AA01165	Human secreted pro	c 505	13.6	14.6	46	22	AA01165	Human secreted pro
c 433	13.6	14.6	28	19	AA01165	Human secreted pro	c 506	13.6	14.6	46	22	AA01165	Human secreted pro
c 434	13.6	14.6	28	19	AA01165	Human secreted pro	c 507	13.6	14.6	46	22	AA01165	Human secreted pro
c 435	13.6	14.6	28	19	AA01165	Human secreted pro	c 508	13.6	14.6	46	22	AA01165	Human secreted pro
c 436	13.6	14.6	28	19	AA01165	Human secreted pro	c 509	13.6	14.6	46	22	AA01165	Human secreted pro
c 437	13.6	14.6	28	19	AA01165	Human secreted pro	c 510	13.6	14.6	46	22	AA01165	Human secreted pro
c 438	13.6	14.6	28	19	AA01165	Human secreted pro	c 511	13.6	14.6	46	22	AA01165	Human secreted pro
c 439	13.6	14.6	28	19	AA01165	Human secreted pro	c 512	13.6	14.6	46	22	AA01165	Human secreted pro
c 440	13.6	14.6	28	19	AA01165	Human secreted pro	c 513	13.6	14.6	46	22	AA01165	Human secreted pro
c 441	13.6	14.6	28	19	AA01165	Human secreted pro	c 514	13.6	14.6	46	22	AA01165	Human secreted pro
c 442	13.6	14.6	28	19	AA01165	Human secreted pro	c 515	13.6	14.6	46	22	AA01165	Human secreted pro
c 443	13.6	14.6	28	19	AA01165	Human secreted pro	c 516	13.6	14.6	46	22	AA01165	Human secreted pro
c 444	13.6	14.6	28	19	AA01165	Human secreted pro	c 517	13.6	14.6	46	22	AA01165	Human secreted pro
c 445	13.6	14.6	28	19	AA01165	Human secreted pro	c 518	13.6	14.6	46	22	AA01165	Human secreted pro
c 446	13.6	14.6	28	19	AA01165	Human secreted pro	c 519	13.6	14.6	46	22	AA01165	Human secreted pro
c 447	13.6	14.6	28	19	AA01165	Human secreted pro	c 520	13.6	14.6	46	22	AA01165	Human secreted pro

Query Match 17.0%; Score 15.8; DB 20; Length 35;
 Best Local Similarity 17.0%; Pred. No. 2.5e+01;
 Matches 17; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 Oy 67 GGGGGCTCCGCAAACTGATGATG 93
 Db 30 GGGGGCTCCGCAAACTGATGATG 4

RESULT 29
 AA28217/C
 ID AA28217 standard; DNM: 39 BP.
 AA28217;
 XX 20-DEC-1999 (first entry)
 DB Mouse splice acceptor sequence #4.
 NM Gene trapping; splicing; integration; mutation; genome; intron; exon;
 NM splice acceptor; identification; ss.
 XX Synthetic.
 OS Mus musculus.
 XX W0950426.1.
 XX 07-OCT-1999.
 XX 26-MAR-1999; 99NO-0506474.
 XX 27-MAR-1999; 98MS-0070728.
 XX 06-APR-1998; 98MS-0057228.
 XX 14-APR-1998; 98MS-0081277.
 XX (LEXI-) LEXICON GENETICS INC.
 XX L24400026 B, Friedrich GA, Sands AT.
 PI WPI: 1999-59134/50.
 XX New gene trapping vectors useful for identifying, activating or
 XX muting genes in eukaryotic cells
 XX
 XX Disclosure: Page 13; 74pp; English.

This sequence represents a murine splice acceptor sequence for use
 in a 5' gene trap cassette. Gene trapping can be used to simultaneously
 identify and inactivate genes in a manner that allows the cellular splicing
 machinery to splice vector-encoded exons to cellular mRNAs. A gene trap
 cassette may comprise a strong splice acceptor sequence, selectable
 marker sequences and a polyadenylation site, but not a promoter.
 Similarly, a cassette may comprise a translation initiation codon and open
 reading frame and/or internal ribosome entry site, a splice donor
 sequence and optionally intronic sequences. After integration of the
 gene trap cassette, the gene trap cassette can be used to acquire novel
 target cell genomes. Such gene trapping can be used to acquire novel
 genes and phenotypes, especially in the analysis of single nucleotide
 polymorphisms or naturally occurring cellular genes, useful to study gene
 function. They can be used to produce mutated cells or animals, and are
 useful in screening, for example, to identify molecules which liberate
 of cells, useful for large scale genetic analysis of the genome and to
 identify novel and mutated genes. The vectors are more efficient (e.g.,
 vectors that rely on gene trapping as detected by antibiotic selection.

CC Use of vectors incorporating 5' gene trap cassette increase the
 CC efficiency of identifying the 5' ends of genes open reading frames,
 CC important because these are difficult to obtain by conventional methods,
 CC and often code for the signal sequence in secreted transmembrane
 CC proteins, an important group for potential drug targets
 XX

Sequence 39 BP; 7 A; 17 C; 7 G; 8 T; 0 other;
 50
 Query Match 17.0%; Score 15.8; DB 20; Length 39;
 Best Local Similarity 17.1%; Pred. No. 2.5e+01;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 67 GGGGGCTCCGCAAACTGATGATG 93
 Db 30 GGGGGCTCCGCAAACTGATGATG 7

RESULT 30
 AAA29286/C
 ID AAA29286 standard; DNM: 39 BP.
 AAA29286;
 XX 12-SEP-2000 (first entry)
 DB Splice acceptor sequence 5 for 5' gene trap cassette.
 NM Splice acceptor; vectors; gene trap; gene discovery; cloning; analysis;
 NM shuttling; gene activation; over-expression; ss.
 XX Synthetic.
 OS Mus musculus.
 XX W020003126.2.
 XX 02-JUN-2000.
 XX 19-MAY-1999; 99NO-0527366.
 XX 20-MAY-1998; 98MS-0109302.
 XX 25-MAR-1999; 99MS-0276533.
 XX (LEXI-) LEXICON GENETICS INC.
 XX L24400026 B, Friedrich GA, Lillberg S, Sands AT.
 PI WPI: 2000-40053/74.
 XX Recombinant vectors for use in, for example, gene discovery, gene
 XX cloning and gene mutation
 XX
 XX Disclosure: Page 13; 74pp; English.

AAA29286-92 are examples of suitable splice acceptor sequences for use
 in construction of genetically informative gene trap cassettes. After
 integration into the host cell genome, enhance the number of cellular
 genes that can be identified and mutated. A gene trap cassette
 the 5A, which encodes a marker enabling the identification of a cell
 expressing the exon and a polyadenylation sequence defining the 3' end
 mutation, gene regulation, shuttling nucleic acid sequences throughout
 the genome and gene activation and over expression. The vectors can be
 used to trap genes that are expressed in the cell type into which the vector
 is incorporated. Cells harboring the vectors can be screened using
 automated gene identification assays such as screening for mutations and
 rapidly identify the mutated or trapped genes.

Sequence 39 BP; 7 A; 17 C; 7 G; 8 T; 0 other;
 50
 Query Match 17.0%; Score 15.8; DB 21; Length 39;

PS Claim 1: Page 44: 108pp: English.

CC AY9900138 represents a human myelin transferase (DNM Wntase) genomic
CC fragment. The sequence length is 108 pp. The sequence is a
CC length sequence AY990138. The sequences can be used to derive antisense
CC oligonucleotides which inhibit DNM Wntase expression. The antisense
CC oligonucleotides can be used to inhibit the growth of the cell
CC in cellular growth. They can be administered at different routes
CC of the cell cycle, or in conjunction with promoters or inhibitors of cell
CC type of interest. The antisense oligonucleotides in the growth of the cell
CC inhibiting tumour growth in a mammal, or to activate attenuated genes to
CC e.g. in beta thalassemia gene function. This ameliorates disease symptoms,
CC oligonucleotides can also be used as analytical and diagnostic tools
CC and a potential source of transgenic plant and animal studies.

Seq Sequence 43 BP: 2 A: 6 C: 13 G: 22 T: 0 other:

Query Match 16.84; Score 15.6; DB 20: Length 43;
Best Local Similarity 70.0%; Read No. 36404

Matches 21: Conservative 0; Mismatches 9; Indels 0; Gaps 0;

07 18 TTTCTCCCTGCGCTGACGCTGCTGCTTCA 47
DB 8 TTTCTCCCTGCGCTGCTGCTGCTTCA 37

RESULT 44

XX AY990138 standard; DNM: 47 BP.

XX AY990138 standard; DNM: 47 BP.

XX AY990138 standard; DNM: 47 BP.

XX AY990138 standard; DNM: 47 BP.

XX AY990138 standard; DNM: 47 BP.

XX AY990138 standard; DNM: 47 BP.

XX AY990138 standard; DNM: 47 BP.

XX AY990138 standard; DNM: 47 BP.

XX AY990138 standard; DNM: 47 BP.

XX AY990138 standard; DNM: 47 BP.

XX AY990138 standard; DNM: 47 BP.

XX AY990138 standard; DNM: 47 BP.

XX AY990138 standard; DNM: 47 BP.

XX AY990138 standard; DNM: 47 BP.

XX AY990138 standard; DNM: 47 BP.

XX AY990138 standard; DNM: 47 BP.

XX AY990138 standard; DNM: 47 BP.

XX AY990138 standard; DNM: 47 BP.

XX AY990138 standard; DNM: 47 BP.

XX AY990138 standard; DNM: 47 BP.

XX AY990138 standard; DNM: 47 BP.

XX AY990138 standard; DNM: 47 BP.

XX AY990138 standard; DNM: 47 BP.

CC AY990138 standard; DNM: 47 BP.

CC AY990138 standard; DNM: 47 BP.

CC AY990138 standard; DNM: 47 BP.

CC AY990138 standard; DNM: 47 BP.

CC AY990138 standard; DNM: 47 BP.

CC AY990138 standard; DNM: 47 BP.

CC AY990138 standard; DNM: 47 BP.

CC AY990138 standard; DNM: 47 BP.

CC AY990138 standard; DNM: 47 BP.

CC AY990138 standard; DNM: 47 BP.

CC AY990138 standard; DNM: 47 BP.

CC AY990138 standard; DNM: 47 BP.

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CC AY990138 standard; DNM: 47 BP.

CC AY990138 standard; DNM: 47 BP.

CC AY990138 standard; DNM: 47 BP.

CC AY990138 standard; DNM: 47 BP.

CC AY990138 standard; DNM: 47 BP.

CC AY990138 standard; DNM: 47 BP.

CC AY990138 standard; DNM: 47 BP.

CC AY990138 standard; DNM: 47 BP.

CC AY990138 standard; DNM: 47 BP.

CC AY990138 standard; DNM: 47 BP.

CC AY990138 standard; DNM: 47 BP.

CC AY990138 standard; DNM: 47 BP.

CC AY990138 standard; DNM: 47 BP.

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CC AY990138 standard; DNM: 47 BP.

CC AY990138 standard; DNM: 47 BP.

CC AY990138 standard; DNM: 47 BP.

CC AY990138 standard; DNM: 47 BP.

CC AY990138 standard; DNM: 47 BP.

CC AY990138 standard; DNM: 47 BP.

CC AY990138 standard; DNM: 47 BP.

CC AY990138 standard; DNM: 47 BP.

CC AY990138 standard; DNM: 47 BP.

CC AY990138 standard; DNM: 47 BP.

CC assays to detect and quantitate the presence of salivary nucleic acids
 CC in samples, and therefore which patients may be in need of further
 CC studies. The invention also provides for the use of the invention in the
 CC production of antibodies specific for polymorphic polypeptides. The
 CC antibodies may also be used to down regulate expression and activity
 CC of the protein. The invention also provides for screening the
 CC presence of polymorphic polypeptides in samples.

XX Sequence 50 BP: 8 A; 16 C; 17 G; 9 T; 0 other:
 50

Query Match 16 84; Score 15.6; DB 22; Length 50;
 Best Local Similarity 70.04; Pval 2e-44;
 Matches 21; Conserved 0; Mismatches 5; Indels 0; Gaps 0;

16 CATTCTCCCTGGTGCACATCCCTTCCTTT 45
 Db 12 CTTGTCCTCCCTGGTGCACATCCCTTCCTTT 41

RESULT 46
 ID AHA46592/
 AHA46592 standard; DNK; 50 BP.
 AC AHA46592;
 XX
 XX 19-OCT-2001 (first entry)
 XX
 XX Human G-protein subunit (beta3) intron 9 DNA fragment 45.
 DE
 XX Human: G-protein subunit (beta3); variant: high blood pressure; asthma;
 XX hypertension; cardiac infarction; coronary disease; heart disease;
 XX circulatory disease; diabetes; psychiatric disease; Crohn's disease;
 XX colitis ulcerosa; transplanted rejection; colitis ulcerosa;
 XX transplanted rejection; diabetes;
 XX
 XX homo sapiens.
 XX
 XX DE10030945-NL.
 XX
 XX PD 05-AUG-2001.
 XX
 XX 24-JUN-2000; 2000DE-1030945.
 XX
 XX 03-FEB-2000; 2000DE-1004681.
 XX
 XX 21-FEB-2000; 2000DE-1007587.
 XX
 XX (STFF)/ SIFFERT W.
 XX
 XX SIFFERT W;
 XX
 XX WPI: 2001-49007/54.
 XX
 XX Use of sequence variants of the beta3 subunit of human G protein to
 XX predict, detect, and determine drug targets for diseases including
 XX heart, immunological, and psychiatric diseases.
 XX
 XX Disclosure: Page 3; 1app; German.

XX This invention describes a novel use for sequence variants of the human
 XX G-protein beta3 subunit to predict physiological and pathological
 XX pathways in the human body. The invention may be used to detect, detect
 XX production of high blood pressure, hypertension, or cardiac infarction, coronary
 XX disease, and other heart or circulatory diseases, diabetes, psychiatric
 XX diseases, immunological diseases, asthma, poor heart health, Crohn's
 XX disease, colitis ulcerosa, transplanted rejection, HIV or protein (beta3) subunit
 XX intron 9 which is used to illustrate the method of the invention.

XX Sequence 50 BP: 14 A; 13 C; 19 G; 4 T; 0 other:
 50

Query Match 16 84; Score 15.6; DB 22; Length 50;
 Best Local Similarity 70.04; Pval 2e-44;
 Matches 21; Conserved 0; Mismatches 5; Indels 0; Gaps 0;

16 CATTCTCCCTGGTGCACATCCCTTCCTTT 45
 Db 40 CACTCTCCCTGGTGCACATCCCTTCCTTCCTTT 11

RESULT 47
 ID AHA46593/
 AHA46593 standard; DNK; 50 BP.
 AC AHA46593;
 XX
 XX 19-OCT-2001 (first entry)
 XX
 XX Human G-protein subunit (beta3) intron 9 DNA fragment 46.
 DE
 XX Human: G-protein subunit (beta3); variant: high blood pressure; asthma;
 XX hypertension; cardiac infarction; coronary disease; heart disease;
 XX circulatory disease; diabetes; psychiatric disease; Crohn's disease;
 XX colitis ulcerosa; transplanted rejection; colitis ulcerosa;
 XX transplanted rejection; diabetes;
 XX
 XX homo sapiens.
 XX
 XX DE10030945-NL.
 XX
 XX PD 05-AUG-2001.
 XX
 XX 24-JUN-2000; 2000DE-1030945.
 XX
 XX 03-FEB-2000; 2000DE-1004681.
 XX
 XX 21-FEB-2000; 2000DE-1007587.
 XX
 XX (STFF)/ SIFFERT W.
 XX
 XX SIFFERT W;
 XX
 XX WPI: 2001-49007/54.
 XX
 XX Use of sequence variants of the beta3 subunit of human G protein to
 XX predict, detect, and determine drug targets for diseases including
 XX heart, immunological, and psychiatric diseases.
 XX
 XX Disclosure: Page 3; 1app; German.

XX This invention describes a novel use for sequence variants of the human
 XX G-protein beta3 subunit to predict physiological and pathological
 XX pathways in the human body. The invention may be used to detect, detect
 XX production of high blood pressure, hypertension, or cardiac infarction, coronary
 XX disease, and other heart or circulatory diseases, diabetes, psychiatric
 XX diseases, immunological diseases, asthma, poor heart health, Crohn's
 XX disease, colitis ulcerosa, transplanted rejection, HIV or protein (beta3) subunit
 XX intron 9 which is used to illustrate the method of the invention.

XX Sequence 50 BP: 15 A; 13 C; 18 G; 4 T; 0 other:
 50

Query Match 16 84; Score 15.6; DB 22; Length 50;
 Best Local Similarity 70.04; Pval 2e-44;
 Matches 21; Conserved 0; Mismatches 5; Indels 0; Gaps 0;

16 CATTCTCCCTGGTGCACATCCCTTCCTTT 45
 Db 40 CACTCTCCCTGGTGCACATCCCTTCCTTCCTTT 11

RESULT 48
 ID AHA50681/
 AHA50681 standard; DNK; 28 BP.
 AC AHA50681;

CC plasmic plasma) which contained the cDNA sequence of the MPP
 CC (Accession: AF010420) and the MPP cDNA sequence of the MPP
 CC completed the nt 299-397 of the sequence in brain at al. 1992.
 CC EMBL J. 11:3219-3227, which codes for the MPP. At Asp 718 cleavage
 CC site, the MPP cDNA sequence is identical to the MPP cDNA
 CC inserted a BamHI site at the 3' end of the sequence.
 XX Sequence 31 BP: 7 A; 8 C; 9 G; 7 T; 0 other;
 SQ
 Query Match 16.6%; Score 15.4; DB 15; Length 31;
 Best Local Similarity 76.0%; Freq. No. 3.2e+04;
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 XY 34 ATGCGCTGGTTCACACACACGCA 58
 DB 7 ATCCCTGCTGGTTCACACACACGCA 31
 RESULT 51
 X AV111984 standard; DNM: 31 BP.
 AC AV111984;
 XX 21-JUL-1998 (first entry)
 XX
 XX
 XX
 DE Potato matrix processing peptidase PCR primer Mito-792.
 XX Acetyl-CoA hydrolase; Acetyl-CoA; AcCoA; transgenic plant;
 XX regulator; control; intracellular distribution; metabolism; acetate;
 XX isoprenoid; steroid; flavonoid; hormone; fat content; PCR primer; 89.
 OS Synthetic.
 OS Solanum tuberosum.
 XX
 XX W0300681-AL
 XX
 XX 19-FEB-1998.
 XX
 XX
 XX 13-AUG-1996; 9606-1032121.
 XX
 XX 08-AUG-1996; 9606-1032121.
 XX
 XX (PLAC) MKN PLANK GRS FOSKERNING WISSENCHAFTEN.
 PI Baeuerlein M, La COGNATA U, Mueller-Roeber B, Willmitzer L;
 WPI: 1998-15956/14.
 XX
 XX Transgenic plants expressing heterologous acetyl-coenzymes A
 XX and B in potato tubers. The transgenic plants were obtained by
 XX distribution of acetyl-coenzymes, specifically for oleaginous plants,
 XX higher fat content in seeds
 XX
 XX Example 1: Page 27; 65pp; German.
 XX
 XX AV11793-V11390 are primers used in a method to construct a transgenic
 XX plant which has higher activity than wild-type cells. Controlling an
 XX hydrolytic activity is used to regulate intracellular distribution of
 XX to altered production of isoprenoids, steroids, flavonoids, hormones,
 XX fats, oils, rubber, alcohols, sugars and starch and anti-pathogenic
 XX (see 7a) of oilseed production is associated with a transgenic
 XX plant which has higher activity than wild-type cells. The method
 XX oil plants, but the method can also be applied to cereals, vegetables,
 XX suggest beet, tobacco, cotton or ornamental plants.
 XX
 XX Sequence 31 BP: 7 A; 8 C; 9 G; 7 T; 0 other;
 SQ
 Query Match 16.6%; Score 15.4; DB 19; Length 31;
 Best Local Similarity 76.0%; Freq. No. 3.2e+04;
 DB

Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 XY 34 ATGCGCTGGTTCACACACACGCA 58
 DB 7 ATCCCTGCTGGTTCACACACACGCA 31
 RESULT 52
 X AV110420 standard; DNM: 31 BP.
 AC AV110420;
 XX 02-JUL-1998 (first entry)
 XX
 XX
 XX
 XX Potato MPP PCR primer Mito-792.
 XX Acetyl-CoA hydrolase; transgenic plant; phenylpropanoid; potato;
 XX altered metabolism; matrix processing peptidase; MPP; PCR primer; 89.
 OS Synthetic.
 OS Solanum tuberosum.
 XX
 XX DE1962121-AL.
 XX
 XX 12-FEB-1998.
 XX
 XX 08-AUG-1996; 9606-1032121.
 XX
 XX 08-AUG-1996; 9606-1032121.
 XX
 XX (PLAC) MKN PLANK GRS FOSKERNING WISSENCHAFTEN.
 PI Baeuerlein M, La COGNATA U, Mueller-Roeber B, Willmitzer L;
 WPI: 1998-121465/13.
 XX
 XX Transgenic plant cells - containing foreign acetyl-CoA hydrolase
 XX gene
 XX
 XX Example 1: Page 10; 26pp; German.
 XX
 XX PCR primers AV10419 & AV10420 are used to amplify the potato matrix
 XX processing peptide (MPP) which is used in a method resulting in the
 XX production of transgenic plants which is used in a method resulting in the
 XX production of transgenic plants which is used in a method resulting in the
 XX wild-type cells as a result of the expression of a foreign DNA sequence
 XX encoding a protein with acetyl-CoA hydrolase activity. The transgenic
 XX plants have higher activity than wild-type cells. The method can also be
 XX increased fatty acid levels in leaves or seeds, increased soluble sugar
 XX levels in leaves, increased starch levels in leaves, reduced growth.
 XX Multiple shoot formation, and change in leaf colour.
 XX
 XX Sequence 31 BP: 7 A; 8 C; 9 G; 7 T; 0 other;
 SQ
 Query Match 16.6%; Score 15.4; DB 19; Length 31;
 Best Local Similarity 76.0%; Freq. No. 3.2e+04;
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 XY 34 ATGCGCTGGTTCACACACACGCA 58
 DB 7 ATCCCTGCTGGTTCACACACACGCA 31
 RESULT 53
 X AA959684 standard; DNM: 39 BP.
 AC AA959684;
 XX 23-JUL-2001 (first entry)
 XX
 XX
 XX Probe used to identify Flay sequences in microorganisms.
 DE

CC amount, so that they are unequivocally identified from mass and from
 CC sequence. The method is simple, quick, automatable and suitable for
 CC (1) is calculated. The method is used for quantitative determination of
 CC RNA and DNA. The method is simple, quick, automatable and suitable for
 CC isophenolomic screening. The method is used for early mental confirmation of
 CC the efficiency of the amplification. This sequence represents a 4
 CC primer used in the amplification of a nucleic acid fragment, using a 4
 CC dehydrogenase (MDH) gene used to illustrate the method of the invention.

XX Sequence 36 BP: 9 A; 10 C; 11 G; 6 T; 0 other:

Query Match 16 34; Score 15.2; DB 22; Length 36;

Best Local Similarity 16 34; Score 15.2; DB 22; Length 36;

Match 21; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

DB 21 7696AACCTTCATCTCC 24

DB 21 7696AACCTTCATCTCC 2

RSR076 65

AB050773

AB050773 standard; DNA; 41 BP.

AB050773;

11-JUN-1999 (first entry)

Brassica sp. polymorphic marker 85/18A1/06 DNA.

polymorphic marker; allele-specific primer; probe: amplification;

hybridisation; plant; hybrid certification; genetic contribution;

progeny; back-cross; hybrid ancestry; ss.

Brassica sp.

Key location/qualifiers

variation 21 34; a "a"

note: "polymorphism"

W0982476-A1.

01-DEC-1997; 97MD-0521782.

07-MAR-1997; 97DS-081307.

02-DEC-1996; 96DS-0024069.

(AFY-) AFRYMETRIX INC.

Landy BS, Lemieux B, Murgueux A, Sopolaky M;

WPI: 1998-31323/75.

Brassica species allele-specific oligonucleotide probes and primers

- useful for plant breeding

Class 1; Page 38; 65pp; English.

This DNA sequence is a region of a Brassica napus or Brassica oleracea
 CC genome which contains a polymorphic marker. This sequence can be used
 CC in the construction of allele-specific primers and probes for
 CC amplification or hybridisation. e.g. to determine common or divergent
 CC of an ancestral plant, to trace the progeny of proprietary plants, in
 CC certification of a hybrid plant or to identify the progeny of a
 CC back-crossed plant with an ancestral plant.

50 Sequence 41 BP: 10 A; 11 C; 8 G; 12 T; 0 other:

Query Match 16 34; Score 15.2; DB 19; Length 41;

Best Local Similarity 16 34; Score 15.2; DB 19; Length 41;

Match 21; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

DB 28 G76AAAGCATTCTCCAAATCTCCATG 63

DB 6 G76AAAGCATTCTCCAAATCTCCATG 41

RSR076 66

AB056120

AB056120 standard; DNA; 41 BP.

AB056120;

22-MAR-2000 (first entry)

Brassica polymorphic site containing sequence 123-85/18A1/16.

plant; polymorphism; single nucleotide polymorphism; SNP;

cruciferae; agriculture; food; canola; condiment; oilseed; vegetable;

ss.

Brassica sp.

Key location/qualifiers

variation 21 34; a "a"

W0515668-A1.

19-MAR-2000.

14-DEC-1999; 99DS-046453.

02-DEC-1996; 96DS-0320697.

(AFY-) AFRYMETRIX INC.

Landy BS, Lemieux B, Sopolaky M;

WPI: 2002-314751/75.

polymorphic oligonucleotides from Brassica napus and B. oleracea useful

for identifying, distinguishing, and determining the relationships of

e.g. canola strains or pools of nucleic acids from cruciferae plants,

Examples: Column 7-8; 40pp; English.

The invention relates to oligonucleotides containing polymorphic

sequences isolated from two Brassica species, B. napus and B. oleracea,

the relationships of individual strains or pools of nucleic acids from

plants within the family Cruciferae. This is useful because many

foodstuffs, for example, condiments, oilseeds, and vegetables, these

include crops such as canola (a type of Brassica napus), which is one of

the largest crops in the world, and Brassica oleracea, which is one of

the largest crops in the world, and Brassica oleracea, which is one of

the largest crops in the world, and Brassica oleracea, which is one of

the largest crops in the world, and Brassica oleracea, which is one of

the largest crops in the world, and Brassica oleracea, which is one of

the largest crops in the world, and Brassica oleracea, which is one of

the largest crops in the world, and Brassica oleracea, which is one of

the largest crops in the world, and Brassica oleracea, which is one of

the largest crops in the world, and Brassica oleracea, which is one of

the largest crops in the world, and Brassica oleracea, which is one of

AAK72187;
 AC AAK7218 standard; RNA; 27 BP.
 XX AAK7218;
 DT 28-JUL-1999 (first entry)
 XX Mouse FLT-1 VEGF receptor hammethead ribozyme #562.
 XX
 XX Vascular endothelial growth factor receptor; VEGF receptor; FLT-1;
 KW FLT-1; KDR; hammethead ribozyme; hairpin ribozyme; cleavage; disease;
 KW VEGF; VEGF receptor; VEGF receptor; VEGF receptor; VEGF receptor;
 KW Ins-Like Tyrosine Kinase I; Kinase insert domain containing receptor;
 KW Fceta1 Liver Kinase I; ss.
 XX
 XX Synthetic.
 OS Mus sp.
 XX W09715602-42.
 XX
 XX PD 01-MAI-1997.
 XX
 XX PE 25-OCT-1996; 96MO-0517480.
 XX
 XX 11-JAN-1995; 95MO-0561010.
 XX 26-OCT-1995; 95MS-0005974.
 XX
 XX (CHIR) CHIRCON CORP.
 XX (RIBO) REBOVIR PHARM INC.
 XX
 XX PT Escobedo J., MCSMajgen J., Ravco P., Stinchcomb D;
 DR WPI: 1997-259017/23.
 XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or
 PT mRNA stability, useful for treating a tumor angiogenesis,
 PT psoriasis, rheumatoid arthritis, etc., in a human patient
 XX
 XX Claim 9; Page 140; 21pp; English.
 XX
 XX The present invention describes nucleic acid molecules which modulate
 CC the expression of nucleic acid molecules which modulate
 CC receptors of vascular endothelial growth factor (VEGF). A patient
 CC (preferably human) having a condition associated with the level of the
 CC receptor (RND) and/or foetal liver kinase I (FLT-1) domain containing
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
 CC be treated by administering the nucleic acid molecule or the expression
 CC vector of the nucleic acid molecule. The nucleic acid molecule or the
 CC vector of the nucleic acid molecule is specific examples
 CC of nucleic acid molecules from the present invention.
 XX
 XX Sequence 27 BP; 9 A; 5 C; 4 G; 8 U; 1 other;
 XX
 XX Query Match 15.9%; Score 14.8; DB 18; Length 27;
 XX Local Similarity 15.9%; Score 14.8; DB 18; Length 27;
 XX Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 OY 61 GGGGCTGCGGACCTCCGAGAAACACT 87
 DB 27 GGGGCTTTCATCATGAAACACT 1

XX
 KW FLT-1; KDR; hammethead ribozyme; hairpin ribozyme; cleavage; disease;
 KW VEGF; VEGF receptor; VEGF receptor; VEGF receptor; VEGF receptor;
 KW Ins-Like Tyrosine Kinase I; Kinase insert domain containing receptor;
 KW Fceta1 Liver Kinase I; ss.
 XX
 XX Synthetic.
 OS Homo sapiens.
 XX W09715602-42.
 XX
 XX PD 01-MAI-1997.
 XX
 XX PE 25-OCT-1996; 96MO-0517480.
 XX
 XX 11-JAN-1995; 95MO-0561010.
 XX 26-OCT-1995; 95MS-0005974.
 XX
 XX (CHIR) CHIRCON CORP.
 XX (RIBO) REBOVIR PHARM INC.
 XX
 XX PT Escobedo J., MCSMajgen J., Ravco P., Stinchcomb D;
 DR WPI: 1997-259017/23.
 XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or
 PT mRNA stability, useful for treating a tumor angiogenesis,
 PT psoriasis, rheumatoid arthritis, etc., in a human patient
 XX
 XX Claim 9; Page 144; 21pp; English.
 XX
 XX The present invention describes nucleic acid molecules which modulate
 CC the expression of nucleic acid molecules which modulate
 CC receptors of vascular endothelial growth factor (VEGF). A patient
 CC (preferably human) having a condition associated with the level of the
 CC receptor (RND) and/or foetal liver kinase I (FLT-1) domain containing
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
 CC be treated by administering the nucleic acid molecule or the expression
 CC vector of the nucleic acid molecule. The nucleic acid molecule or the
 CC vector of the nucleic acid molecule is specific examples
 CC of nucleic acid molecules from the present invention.
 XX
 XX Sequence 27 BP; 9 A; 5 C; 4 G; 8 U; 1 other;
 XX
 XX Query Match 15.9%; Score 14.8; DB 18; Length 27;
 XX Local Similarity 15.9%; Score 14.8; DB 18; Length 27;
 XX Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 OY 61 GGGGCTGCGGACCTCCGAGAAACACT 87
 DB 27 GGGGCTTTCATCATGAAACACT 1

RESULT 96
 AAK709097C
 XX AAK70909 standard; RNA; 27 BP.
 AC AAK70909;
 XX 28-JUL-1999 (first entry)
 XX Human KDR VEGF receptor hammethead ribozyme #581.
 XX
 XX Vascular endothelial growth factor receptor; VEGF receptor; FLT-1;

XX
 DE Primer for calobiohydrolase coding sequence.
 KW Calobiohydrolase; CMB A; CMB B; cellulase degradation; food production;
 KW beverage production; animal feed production; endoglucanase; PCR primer;
 XX
 XX Synthetic.
 OS Aspergillus niger.
 XX W09906574-41.
 XX 11-FEB-1999.

XX NMFI: 1999-080943/07.
 XX New nucleic acid sequence containing polymorphic sites - used for
 XX e.g. detecting a disease phenotype (e.g. consensu), identifying
 XX or genetic mapping of phenotypic traits
 XX Claim 1: page 15; 61pp English
 XX
 XX Sequence AMX0101-206558 represent human DNA fragments which contain
 XX polymorphic sites
 XX 15 indicated by the appropriate IUPAC-ambiguity code polymorphic site
 XX medium for storing data for use in a computer-readable storage
 XX executed on a data processing system. Such a method comprises a data
 XX structure stored in the computer-readable storage medium, the data
 XX application program and including records, each record comprising
 XX information identifying a polymorphism shown in the above sequences. The
 XX individuals for testing for the presence of a disease phenotype or in
 XX for forensic, paternity testing or genetic mapping of phenotypic traits.
 XX variant genes and for the production of polypeptides expressed by
 XX acid segments can also be used in the manufacture of medicaments for the
 XX treatment or prophylaxis of diseases.
 XX Sequence 31 BP: 8 A; 6 C; 8 G; 8 T; 1 other:
 XX
 XX Query Match 15 94; Score 14.8; DP 16; Length 31;
 XX Best Local Similarity 67.94; Pred. No. 5.4e+04;
 XX Matches 19; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
 XX
 XX 13 CTTCAATCTCTCTGGGTGACATGCTT 40
 XX 31 CTTCAATCTCTCTGGGTGACATGCTT 4
 XX
 XX RESUME 110
 XX AMX0101-206558
 XX ID AMX0552 standard: DNA; 36 BP.
 XX
 XX AMX0552;
 XX
 XX 11-JUL-1997 (first entry)
 XX
 XX Progesterin regulated gene 1 (PRG1) reverse primer.
 XX
 XX Progesterin-regulated gene 1; PRG1; breast cancer; LNCaP; T-47D;
 XX progesterin-regulated gene 1; PRG1; breast cancer; LNCaP; T-47D;
 XX antiproliferative gene therapy; polyomerase chain reaction; PCR;
 XX primer; 88.
 XX
 XX Synthetic.
 XX
 XX NMW0915674-AL.
 XX
 XX 01-MAY-1997.
 XX
 XX 24-OCT-1996; 96AG-A000669.
 XX
 XX 19-JUL-1996; 96AG-0001128.
 XX
 XX 24-OCT-1995; 95AG-0006144.
 XX
 XX (GARY) GARYAN INST MEDICAL RES.
 XX
 XX Hamilton 3A; WATTS CMV;
 XX
 XX NMFI: 1997-25906/23.
 XX
 XX Progesterin-regulated gene - indicative of a subject's progesterin
 XX responsiveness, also for treatment of metabolic disease or

XX hyperproliferation etc
 XX Example: page 14; 50pp English.
 XX
 XX A forward primer (AMX0551) and reverse primer (AMX0552) were used
 XX to generate a full-length open reading frame of the novel human
 XX progesterin-regulated gene PRG1 (see also AMX0548) contg. LNCaP
 XX bacterial expression vector pRAC42-2 to produce a pool of PRG1
 XX polypeptides (see also AMX1547) as a soluble fusion protein in
 XX Escherichia coli O15A transformants.
 XX
 XX Sequence 36 BP: 7 A; 9 C; 10 G; 10 T; 0 other:
 XX
 XX Query Match 15 94; Score 14.8; DP 16; Length 36;
 XX Best Local Similarity 88.94; Pred. No. 5.7e+04;
 XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 XX
 XX 73 CTTCAATCTCTCTGGGTGAC 90
 XX 29 CTTCAATCTCTCTGGGTGAC 12
 XX
 XX Search completed: July 5, 2003, 12:29:25
 XX 500 time; 216 secs

The first part of the paper discusses the importance of maintaining accurate records of all transactions. It is essential for the business to have a clear and concise record of all income and expenses. This will allow the business to track its financial performance over time and identify areas for improvement.

The second part of the paper discusses the importance of maintaining accurate records of all assets and liabilities. This will allow the business to track its net worth over time and identify areas for improvement.

The third part of the paper discusses the importance of maintaining accurate records of all debts and obligations. This will allow the business to track its financial obligations over time and identify areas for improvement.

The fourth part of the paper discusses the importance of maintaining accurate records of all taxes and other legal obligations. This will allow the business to track its financial obligations over time and identify areas for improvement.

The fifth part of the paper discusses the importance of maintaining accurate records of all other financial information. This will allow the business to track its financial performance over time and identify areas for improvement.

Genomic version 5.1.6
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CM nucleic - nucleic search, using sz model

Run on: July 5, 2003, 04:20:39, Search time 905 seconds

(without alignments) 2747.779 Million cell updates/sec

Title: US-09-843-377-3_COPY_1000_1092

Percent score: 1 gagectygaagcaccacaccc.....ctccgaagacatgagag 93

Sequence: 1 gagectygaagcaccacaccc.....ctccgaagacatgagag 93

Scoring table: IDENTITY -0.05, Gapset 1.0

Searches: 2054640 steps, 1455102877 residues

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum March 08
Maximum March 1008

Listing first 1000 summaries

Database : Genbank
1: gb-bat*
2: gb-bat*
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9: gb-bat*
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63: gb-bat*
64: gb-bat*
65: gb-bat*

Score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Length	DB	ID	Description
	1	18.6	20.0	45	6	AB078468	AB078468 Sequence
	2	17.2	18.5	50	6	AB149380	AB149380 Sequence
	3	16.8	18.1	30	6	AB159154	AB159154 Sequence
	4	16.6	17.8	30	6	AB093240	AB093240 Sequence
	5	16.6	17.8	34	11	U757053	U757053 Sequence
	6	16.6	17.8	34	11	U757053	U757053 Sequence
	7	16.6	17.8	34	11	U757053	U757053 Sequence
	8	16.6	17.8	34	11	U757053	U757053 Sequence
	9	16.6	17.8	34	11	U757053	U757053 Sequence
	10	16.6	17.8	34	11	U757053	U757053 Sequence
	11	16.2	17.4	48	9	AB149118	AB149118 Sequence
	12	16.2	17.4	48	9	AB149118	AB149118 Sequence
	13	16.2	17.4	48	9	AB149118	AB149118 Sequence
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	15	16.2	17.4	48	9	AB149118	AB149118 Sequence
	16	16.2	17.4	48	9	AB149118	AB149118 Sequence
	17	16.2	17.4	48	9	AB149118	AB149118 Sequence
	18	16.2	17.4	48	9	AB149118	AB149118 Sequence
	19	16.2	17.4	48	9	AB149118	AB149118 Sequence
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	25	16.2	17.4	48	9	AB149118	AB149118 Sequence
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	28	16.2	17.4	48	9	AB149118	AB149118 Sequence
	29	16.2	17.4	48	9	AB149118	AB149118 Sequence
	30	16.2	17.4	48	9	AB149118	AB149118 Sequence
	31	16.2	17.4	48	9	AB149118	AB149118 Sequence
	32	16.2	17.4	48	9	AB149118	AB149118 Sequence
	33	16.2	17.4	48	9	AB149118	AB149118 Sequence
	34	16.2	17.4	48	9	AB149118	AB149118 Sequence
	35	16.2	17.4	48	9	AB149118	AB149118 Sequence
	36	16.2	17.4	48	9	AB149118	AB149118 Sequence
	37	16.2	17.4	48	9	AB149118	AB149118 Sequence
	38	16.2	17.4	48	9	AB149118	AB149118 Sequence
	39	16.2	17.4	48	9	AB149118	AB149118 Sequence
	40	16.2	17.4	48	9	AB149118	AB149118 Sequence
	41	16.2	17.4	48	9	AB149118	AB149118 Sequence
	42	16.2	17.4	48	9	AB149118	AB149118 Sequence
	43	16.2	17.4	48	9	AB149118	AB149118 Sequence
	44	16.2	17.4	48	9	AB149118	AB149118 Sequence
	45	16.2	17.4	48	9	AB149118	AB149118 Sequence
	46	16.2	17.4	48	9	AB149118	AB149118 Sequence
	47	16.2	17.4	48	9	AB149118	AB149118 Sequence
	48	16.2	17.4	48	9	AB149118	AB149118 Sequence
	49	16.2	17.4	48	9	AB149118	AB149118 Sequence
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	51	16.2	17.4	48	9	AB149118	AB149118 Sequence
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	58	16.2	17.4	48	9	AB149118	AB149118 Sequence
	59	16.2	17.4	48	9	AB149118	AB149118 Sequence
	60	16.2	17.4	48	9	AB149118	AB149118 Sequence
	61	16.2	17.4	48	9	AB149118	AB149118 Sequence
	62	16.2	17.4	48	9	AB149118	AB149118 Sequence
	63	16.2	17.4	48	9	AB149118	AB149118 Sequence
	64	16.2	17.4	48	9	AB149118	AB149118 Sequence
	65	16.2	17.4	48	9	AB149118	AB149118 Sequence

[illegible]

ACCESSION AB051493
 VERSION AB051493.1 GI:5974857
 DEFINITION Unclassified.
 LOCUS unknown.
 ORGANISM unknown.
 REFERENCE 1) de la Monte, S. and Wanda, J.R.
 AUTHORS de la Monte, S. and Wanda, J.R.
 TITLE Neural thread protein gene expression and detection of Alzheimer's
 JOURNAL Disease US 5816670.4 63 03-MAY-1998;
 FEATURES
 source
 1. 31
 ORIGIN
 BASE COUNT 6 a 10 c 8 g 7 t
 Query Match 16.3% Score 15.2; DB 6; Length 31;
 Best Local Similarity 85.0% Pred. No. 5.8e+05;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 DB 18 TTCTCCGCTGGTGCACATGC 37
 27 TTTCTCCGCTGGTGCACATGC 8

ACCESSION AB072633
 VERSION AB072633.1 GI:9993937
 DEFINITION Sequence 63 from patent US 5948634.
 LOCUS 31 bp, DNA linear PAT 28-MAY-2000
 ORGANISM unknown.
 REFERENCE 1) (base 1 to 31)
 AUTHORS Unknown.
 TITLE Disease US 5485974.53 07-SEP-1999;
 JOURNAL Patent: Location/Qualifiers
 FEATURES
 source
 1. 31
 ORIGIN
 BASE COUNT 6 a 10 c 8 g 7 t
 Query Match 16.3% Score 15.2; DB 6; Length 31;
 Best Local Similarity 85.0% Pred. No. 5.8e+05;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 DB 18 TTCTCCGCTGGTGCACATGC 37
 27 TTTCTCCGCTGGTGCACATGC 8

ACCESSION AB072178
 VERSION AB072178.1 GI:9999941
 DEFINITION Sequence 63 from patent US 5948888.
 LOCUS 31 bp, DNA linear PAT 28-MAY-2000
 ORGANISM unknown.
 REFERENCE 1) (base 1 to 31)
 AUTHORS Unknown.
 TITLE Disease US 5488884.53 07-SEP-1999;
 JOURNAL Patent: Location/Qualifiers
 FEATURES
 source
 1. 31

ACCESSION A024615
 VERSION A024615.1 GI:15963238
 DEFINITION Sequence 694 from Patent WO016800.
 LOCUS 31 bp, DNA linear PAT 28-SEP-2001
 ORGANISM human.
 REFERENCE 1) Menzies, J. et al.
 AUTHORS Menzies, J.; Richards, P.; Pringle, C.; Carstairs, J.; Houlden, H.;
 TITLE Human single nucleotide polymorphism
 JOURNAL Human Molecular Genetics 10 13-SEP-2001
 FEATURES
 source
 1. 31
 ORIGIN
 BASE COUNT 6 a 6 c 13 g 5 t
 Query Match 16.3% Score 15.2; DB 6; Length 31;
 Best Local Similarity 85.0% Pred. No. 5.8e+05;
 Matches 17; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 DB 15 CACTTCTCCGCTGGTGCACATGC 36
 22 CACTTCTCCGCTGGTGCACATGC 1

ACCESSION A024615
 VERSION A024615.1 GI:15963238
 DEFINITION Sequence 694 from Patent WO016800.
 LOCUS 31 bp, DNA linear PAT 28-SEP-2001
 ORGANISM human.
 REFERENCE 1) Menzies, J. et al.
 AUTHORS Menzies, J.; Richards, P.; Pringle, C.; Carstairs, J.; Houlden, H.;
 TITLE Human single nucleotide polymorphism
 JOURNAL Human Molecular Genetics 10 13-SEP-2001
 FEATURES
 source
 1. 31
 ORIGIN
 BASE COUNT 6 a 6 c 13 g 5 t
 Query Match 16.3% Score 15.2; DB 6; Length 31;
 Best Local Similarity 85.0% Pred. No. 5.8e+05;
 Matches 17; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 DB 15 CACTTCTCCGCTGGTGCACATGC 36
 22 CACTTCTCCGCTGGTGCACATGC 1

ACCESSION A024615
 VERSION A024615.1 GI:15963238
 DEFINITION Sequence 694 from Patent WO016800.
 LOCUS 31 bp, DNA linear PAT 28-SEP-2001
 ORGANISM human.
 REFERENCE 1) Menzies, J. et al.
 AUTHORS Menzies, J.; Richards, P.; Pringle, C.; Carstairs, J.; Houlden, H.;
 TITLE Human single nucleotide polymorphism
 JOURNAL Human Molecular Genetics 10 13-SEP-2001
 FEATURES
 source
 1. 31
 ORIGIN
 BASE COUNT 6 a 6 c 13 g 5 t
 Query Match 16.3% Score 15.2; DB 6; Length 31;
 Best Local Similarity 85.0% Pred. No. 5.8e+05;
 Matches 17; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 DB 15 CACTTCTCCGCTGGTGCACATGC 36
 22 CACTTCTCCGCTGGTGCACATGC 1

QY 46 CACCTCTTCGCGAT 60
DB 1 CACCTCTTCGCGAT 15

RESULT 41
116731/c
DEFINITION Sequence 8 from patent US 547926.
ACCESSION 116731
VERSION 116731.1 GI:1251639
SOURCE unknown

ORGANISM unknown
FEATURES
REFERENCE 1 (bases 1 to 29)
AUTHORS Spiegelman, B.M., Graves, R., and Ross, S.
TITLE Adipocyte-specific DNA sequences and use thereof in the production of transgenic animals
JOURNAL Patent: US 547926-A, 8-DEC-1995;
LOCATION/Qualifiers Location/Qualifiers

BASE COUNT 9 a 8 4 c 7 g 5 t
ORIGIN

Query Match 16.1% Score 15; DB 6; Length 29;
Best Local Similarity 19.3%; Pred. No. 6;e+05;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 11 CACCTCTTCGCGCGATCA 33
DB 24 CACCTCTTCGCGCGATCA 2

RESULT 42
AC249653
DEFINITION Sequence 1732 from Patent WO016800.
ACCESSION AC249653
VERSION AC249653.1 GI:15864276
SOURCE human

ORGANISM Homo sapiens
Chromosomes: Chromosomes; Contigs: Contigs; Vertebrates: Eumetazoa; Mammalia: Eutheria; Primates: Catarrhini; Hominidae: Homo.
REFERENCE 1 (bases 1 to 31)
AUTHORS Gargiula, M., Ibrahim, J.S. and Landre, R.S.
TITLE Human adipocyte-specific DNA sequences and use thereof in the production of transgenic animals
JOURNAL Patent: WO 016800-A, 1732, 13-SEP-2001;
WHITHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
LOCATION/Qualifiers Location/Qualifiers

BASE COUNT 8 a 10 c 7 g 9 5 t
ORIGIN

Query Match 16.1% Score 15; DB 6; Length 31;
Best Local Similarity 22.0%; Pred. No. 6;e+05;
Matches 18; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 28 GTGCAATCGCTGGTTCACAC 52
DB 28 GTGCAATCGCTGGTTCACAC 4

RESULT 43
AB085045
LOCUS AB085045
DEFINITION Sequence 7 from patent US 5981262.
ACCESSION AB085045.1 GI:10018186
VERSION

KEYWORDS
ORGANISM unknown
REFERENCE 1 (bases 1 to 32)
AUTHORS Brodeur, J., Morganster, J., Shue, L., Zydomsky, L., Zoller, M., and Paeon, A.
TITLE Human 5' US 5981262-A, 7-09-NOV-1999;
JOURNAL Patent: US 5981262-A, 7-09-NOV-1999;
FEATURES
SOURCE 1. 32'uslm50'unknown'
ORIGIN

BASE COUNT 6 a 11 c 4 g 7 t
ORIGIN

Query Match 16.1% Score 15; DB 6; Length 32;
Best Local Similarity 75.0%; Pred. No. 6;e+05;
Matches 15; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 28 GTGCAATCGCTGGTTCAC 47
DB 32 GTGCAATCGCTGGTTCAC 13

RESULT 44
116735/c
LOCUS 116735
DEFINITION Sequence 12 from patent US 547926.
ACCESSION 116735
VERSION 116735.1 GI:1251643
SOURCE unknown

ORGANISM unknown
REFERENCE 1 (bases 1 to 33)
AUTHORS Spiegelman, B.M., Graves, R., and Ross, S.
TITLE Adipocyte-specific DNA sequences and use thereof in the production of transgenic animals
JOURNAL Patent: US 547926-A, 8-DEC-1995;
LOCATION/Qualifiers Location/Qualifiers

BASE COUNT 9 a 8 10 g c 6 t
ORIGIN

Query Match 16.1% Score 15; DB 6; Length 33;
Best Local Similarity 78.3%; Pred. No. 7;e+05;
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RESULT 45
AB127205
LOCUS AB127205
DEFINITION Sequence 9 from patent US 6180391.
ACCESSION AB127205.1 GI:1411798
VERSION
KEYWORDS
ORGANISM unknown
REFERENCE 1 (bases 1 to 36)
AUTHORS Brodeur, J., Morganster, J., Shue, L., Zydomsky, L., Zoller, M., and Paeon, A.
TITLE Human 5' US 6180391-A, 9-30-JUN-2001;
JOURNAL Patent: US 6180391-A, 9-30-JUN-2001;
FEATURES
SOURCE 1. 36'uslm50'unknown'
ORIGIN

BASE COUNT 8 a 10 8 g 12 t

BASE COUNT 13 a 12 c 3 g 13 t
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 Query Match 16.1% Score 15; DB 6; Length 42;
 Best Local Similarity 67.7% Pred. No. 7.2e+05;
 Matches 21: Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 33 AMCCCTGCTTCCTGCGTCCGACATCCGCTG 63
 40 ATCCCTGATATTATGATGATGATGATGATG 10
 DB
 RESULT 51
 LOCUS AB17420 41 bp DNA linear PAT 17-DEC-2001
 DEFINITION Sequence 38 from patent US 6306649.
 VERSION AB17420.1 GI:17915470
 FEATURES
 KEYWORDS
 ORGANISM Unknown.
 SOURCE
 REFERENCE 1 (bases 1 to 41)
 TITLE Heterologous expression factors
 JOURNAL Patent: US 6306649-A 10-23-OCT-2001.
 FEATURES
 SOURCE Location/Qualifiers
 BASE COUNT 16 a 6 c 13 g 6 t
 ORIGIN
 Query Match 16.1% Score 15; DB 6; Length 41;
 Best Local Similarity 67.7% Pred. No. 7.2e+05;
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 45 TCCACATCCGACGATGATCCGCTCCGCTG 75
 5 TCCACATCCGACGATGATCCGCTCCGCTG 35
 DB
 RESULT 52
 LOCUS AB03895 42 bp DNA linear PAT 29-SEP-1999
 DEFINITION Sequence 38 from patent US 5865710.
 VERSION AB03895.1 GI:5949500
 FEATURES
 KEYWORDS
 ORGANISM Unknown.
 SOURCE
 REFERENCE 1 (bases 1 to 42)
 TITLE Rhoads P.R., Jiao J.-A., Burkhardt M. and Wong H.C.
 JOURNAL Patent: US 5865710-A 09-SEP-1999.
 FEATURES
 SOURCE Location/Qualifiers
 BASE COUNT 6 a 20 c 11 g 5 t
 ORIGIN
 Query Match 16.1% Score 15; DB 6; Length 42;
 Best Local Similarity 67.7% Pred. No. 7.2e+05;
 Matches 21: Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 11 CACTCATTCCTGCTGCTGACATCCGCTG 41
 1 CACTCATTCCTGCTGCTGACATCCGCTG 31
 DB
 RESULT 53
 LOCUS AB175028 42 bp DNA linear PAT 17-DEC-2001
 DEFINITION Sequence 38 from patent US 6306649.
 VERSION AB175028
 FEATURES
 KEYWORDS
 ORGANISM Unknown.
 SOURCE
 REFERENCE 1 (bases 1 to 42)
 TITLE HMC molecules and uses thereof
 JOURNAL Patent: US 6306649-A 10-23-OCT-2001.
 FEATURES
 SOURCE Location/Qualifiers
 BASE COUNT 6 a 20 c 11 g 5 t
 ORIGIN
 Query Match 16.1% Score 15; DB 6; Length 42;
 Best Local Similarity 67.7% Pred. No. 7.2e+05;
 Matches 21: Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 11 CACTCATTCCTGCTGCTGACATCCGCTG 41
 1 CACTCATTCCTGCTGCTGACATCCGCTG 31
 DB
 RESULT 54
 LOCUS AB032460 42 bp DNA linear PAT 20-SEP-2000
 DEFINITION Sequence 38 from patent EP0997477.
 VERSION AB032460
 FEATURES
 KEYWORDS
 ORGANISM Unknown.
 SOURCE
 REFERENCE 1 (bases 1 to 42)
 TITLE Rhoads P.R., Jiao J.-A., Burkhardt M. and Wong H.C.
 JOURNAL Patent: EP0997477 03-MAY-2000;
 SOURCE Location/Qualifiers
 BASE COUNT 6 a 20 c 11 g 5 t
 ORIGIN
 Query Match 16.1% Score 15; DB 6; Length 42;
 Best Local Similarity 67.7% Pred. No. 7.2e+05;
 Matches 21: Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 11 CACTCATTCCTGCTGCTGACATCCGCTG 41
 1 CACTCATTCCTGCTGCTGACATCCGCTG 31
 DB
 RESULT 55
 LOCUS AB161438 43 bp DNA linear PAT 17-OCT-2001
 DEFINITION Sequence 33 from patent US 6259462.
 VERSION AB161438
 FEATURES
 KEYWORDS
 ORGANISM Unknown.
 SOURCE
 REFERENCE 1 (bases 1 to 43)
 TITLE Reptide tag for immunodepletion and immunopurification
 JOURNAL Patent: US 6259462 17-OCT-2001.
 FEATURES
 SOURCE Location/Qualifiers


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ARI9590/c
LOCUS ARI9590 5068 from patent US 6346398. 27 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence
VERSION ARI9590.1 GI:203555
KEYWORDS
SOURCE unknown.
ORGANISM unknown.
REFERENCE 1 (bases 1 to 27)
  Stincomb D, and Escobedo J
  Method and reagent for the treatment of diseases or conditions
  related to levels of vascular endothelial growth factor receptor
  protein. Patent: US 6346398 (2002).
  Location/Qualifiers
    1..27
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Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
61 GTGACGTCGCGCCCGGAAACACT 87
27 GTGACGTCGTCACCGAAACACT 1
DB

RESULT 61
LOCUS ARI00160 27 bp DNA linear PAT 10-MAR-2000
DEFINITION Sequence 11 from Patent WO960574.
VERSION ARI00160.1 GI:7240674
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 27)
  Cullis, J.
  CELLULAR DEGRADING ENZYMES OF ASPERGILLUS
  TITLE Patent: WO 960574-A 11 FEB-1999;
  JOURNAL MYCOSIS METHODS CATALAN (M)
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Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
31 AACACCGCTGGCTTCACACATCG 56
2 AACACCGCTTCACACATCG 27
DB

RESULT 62
LOCUS ARI08544 30 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 33 from Patent US 5985599.
VERSION ARI08544.1 GI:10013310
KEYWORDS
SOURCE unknown.
ORGANISM unknown.
REFERENCE 1 (bases 1 to 30)
  McGeer, J.F.C., Bogarth, M.P., Hides, M.L., Scott, B.M., Bonadonna, L.,
  and Bulech, M.D.
  FC receptor for tumorigenesis
  JOURNAL Patent: US 5985599-A 3-16-NOV-1999;
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      /organism="unknown"
BASE COUNT 8 a 6 c 7 g 9 t
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Best Local Similarity 73.11; Pred. No. 8.2e05;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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3 TCCACACATCGCCACGACATCGTC 28
DB

RESULT 63
LOCUS ARI04592/c 36 bp DNA linear PAT 22-SEP-2000
DEFINITION Sequence 9 from Patent EP0685495.
VERSION ARI04592.1 GI:10018185
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
  Hants, C.K., and Hamilton, J.A.
  Progesterin-regulated gene
  TITLE Patent: EP 0685495-A 5-29-SEP-1998;
  JOURNAL GENEVA
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        /db_xref="taxon:3250"
        /note="PCR oligonucleotide primer"
BASE COUNT 7 a 10 g 10 g
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Best Local Similarity 88.34; Pred. No. 8.4e05;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
73 CCGCCGAAACCTTGG 90
29 CCGCCGAAACCTGAG 12
DB

RESULT 64
LOCUS ARI07350 36 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 12 from Patent WO024939.
VERSION ARI07350.1 GI:21440955
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
  Bruch, R., Koenen, Thibaut R., and Lahan, N.
  A method for the production of monoclonal for
  biotechnological and therapeutic applications
  TITLE Patent: WO 024939-A 12-28-MAR-2002;
  JOURNAL research Authority for Applied Research & Industrial Dev
  LTD. (U)
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BASE COUNT 9 a 11 c 15 g 4 t
ORIGIN

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Best Local Similarity: 88.9% Pred. No. gaps: 0;
Matches 15: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 56 GGAATTCATCTCTCCGCG 73
Db 4 GGAATTCATCTCTCCGCG 21

RESULT 76
AA003680.1 21 bp DNA linear PAT 24-MAR-2000
DEFINITION Sequence 1 from Patent WO9727951.
ACCESSION AA003680
VERSION AA003680.1 GI:91927467
SOURCE GenBank
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 21).
AUTHORS De L.L. and La T.N.
TITLE Full length, functional, force-interacting protein and its use
JOURNAL LOMA STRAIN DE (GB); THAMMIE MICHAELAS BARRIE (GB)
FEATURES
source
/organism="synthetic construct"
/db_xref="taxon:37630"

BASE COUNT 4 a 5 c 6 g 7 t
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Best Local Similarity 81.0% Pred. No. gaps: 0;
Matches 17: Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 67 GTGGGCTCTCAAAACAT 87
Db 21 GTGGGCTCTCAAAACAT 1

RESULT 77
AA014977.1 30 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 3730 from Patent WO0129262.
ACCESSION AA014977
VERSION AA014977.1 GI:14035558
SOURCE GenBank
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 21).
AUTHORS Hapshamm, R., Weindl, P., Duerkin-Bastl, E., Adolfs, G.D., Snelly, P.,
TITLE Genetic sequences, type I interferon peptide coded by them, and
JOURNAL these organisms producing the same
PUBLISHED IN PATENT WO 01/29262-3 3730 26-APR-2001;
ORIGIN Orchard Biotechnology, Inc.
FEATURES
source
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BASE COUNT 4 a 5 c 6 g 7 t
ORIGIN
Query Match 15.7% Score 14.6; DB 6; Length 21;
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Matches 17: Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 71 GGGCTCGAAGACCTTGGG 91
Db 21 GGGCTCGAAGACCTTGGG 1

RESULT 78

AA1495 30 bp DNA linear PAT 01-DEC-1993
DEFINITION Nucleotide sequence 35 from patent number EP0170204.
ACCESSION AA1495
VERSION AA1495.1 GI:492479
SOURCE GenBank
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 30).
AUTHORS Duerkin-Bastl, E., Adolfs, G.D., Snelly, P.,
TITLE Genetic sequences, type I interferon peptide coded by them, and
JOURNAL these organisms producing the same
PUBLISHED IN PATENT WO 01/29262-3 35 26-APR-2001;
ORIGIN Orchard Biotechnology, Inc.
FEATURES
source
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/db_xref="taxon:37644"

BASE COUNT 6 a 7 c 9 g 8 t
ORIGIN
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Best Local Similarity 81.0% Pred. No. gaps: 0;
Matches 17: Conservative 0; Mismatches 4; Indels 0; Gaps 0;

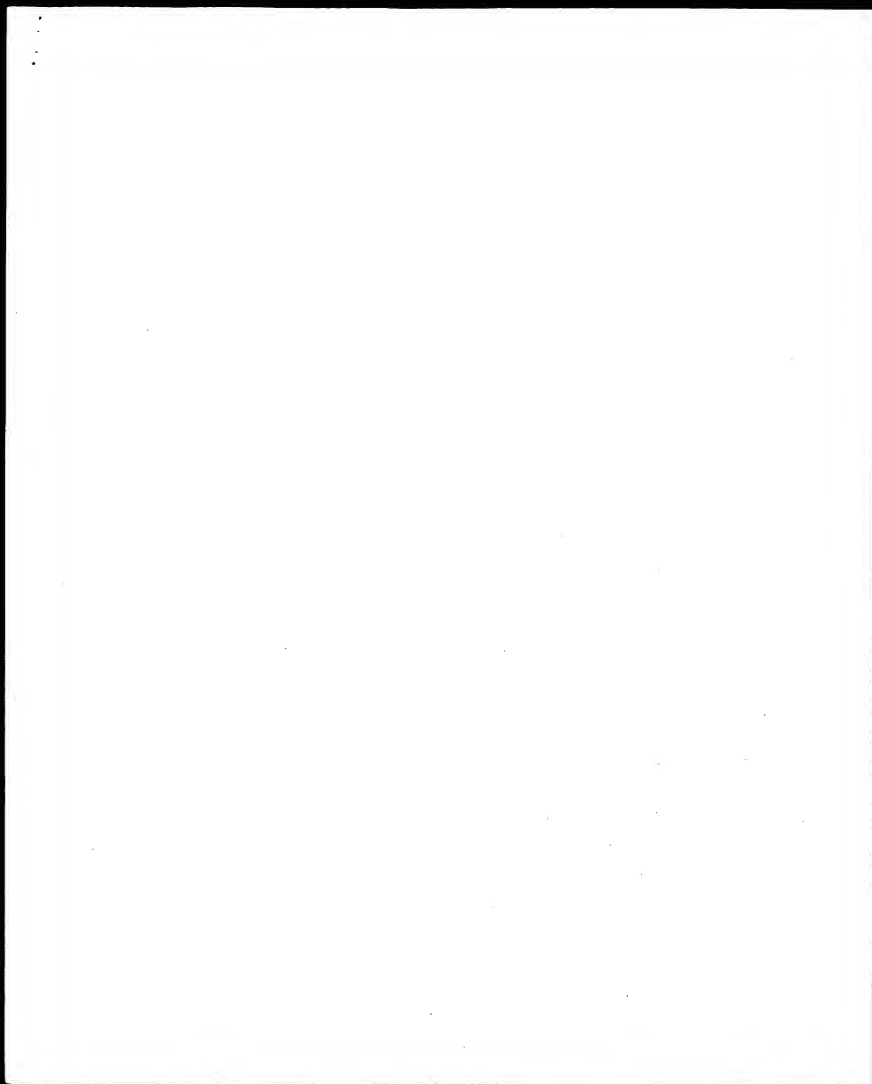
QY 8 GAGGCTCATCTCTCCGCG 28
Db 10 GAGGCTCATCTCTCCGCG 30

RESULT 79
AA1499 30 bp DNA linear PAT 01-DEC-1993
DEFINITION Nucleotide sequence 39 from patent number EP0170204.
ACCESSION AA1499
VERSION AA1499.1 GI:492483
SOURCE GenBank
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 30).
AUTHORS Hapshamm, R., Weindl, P., Duerkin-Bastl, E., Adolfs, G.D., Snelly, P.,
TITLE Genetic sequences, type I interferon peptide coded by them, and
JOURNAL these organisms producing the same
PUBLISHED IN PATENT WO 01/29262-3 39 26-APR-2001;
ORIGIN Orchard Biotechnology, Inc.
FEATURES
source
/organism="unidentified"
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BASE COUNT 6 a 7 c 9 g 8 t
ORIGIN
Query Match 15.7% Score 14.6; DB 6; Length 30;
Best Local Similarity 81.0% Pred. No. gaps: 0;
Matches 17: Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 GAGGCTCATCTCTCCGCG 28
Db 10 GAGGCTCATCTCTCCGCG 30

RESULT 80
AA1501 30 bp DNA linear PAT 01-DEC-1993
DEFINITION Nucleotide sequence 41 from patent number EP0170204.
ACCESSION AA1501
VERSION AA1501.1 GI:492485
SOURCE GenBank
ORGANISM unidentified.



[illegible]

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532	13	14.0	25	05-10-108-2639-336	Sequence 3189, Ap	605	13	14.0	50	05-09-026-819-1135	Sequence 136, Ap	605	13	14.0	50	05-09-026-819-1135	Sequence 136, Ap
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538	13	14.0	25	05-10-108-2639-336	Sequence 5394, A	611	13	14.0	50	05-09-032-819-1135	Sequence 142, Ap	611	13	14.0	50	05-09-032-819-1135	Sequence 142, Ap
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545	13	14.0	25	05-10-108-2639-336	Sequence 9911, A	618	13	14.0	50	05-09-039-819-1135	Sequence 149, Ap	618	13	14.0	50	05-09-039-819-1135	Sequence 149, Ap
546	13	14.0	25	05-10-108-2639-336	Sequence 9912, A	619	13	14.0	50	05-09-040-819-1135	Sequence 150, Ap	619	13	14.0	50	05-09-040-819-1135	Sequence 150, Ap
547	13	14.0	25	05-10-108-2639-336	Sequence 9913, A	620	13	14.0	50	05-09-041-819-1135	Sequence 151, Ap	620	13	14.0	50	05-09-041-819-1135	Sequence 151, Ap
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[illegible]


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			Gaps	0
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Query Match      12.2%  Score 16;  DB 9;  Length 50;
Best Local Similarity 66.7%  Pred. No. 1.35+04;
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DB      11  00666666CCGAGAACATCCAGG665 34

RESULT 6
US-10-098-2638-78554
GENERAL INFORMATION: Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: 05/10/008,2638
PRIOR FILING DATE: 2001-03-16
SOFTWARE: MICROARRAY; PROBE
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 78554
LENGTH: 25
ORGANISM: Homo sapien
US-10-098-2638-78554
Query Match
Best Local Similarity 17.0% Score 15.8; DB 9; Length 35;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
DB      2  26606666CCTCCAGAACAC 20

RESULT 7
US-10-158-735-10/C
Sequence 10, Application US/0158735
Publication No. US20030182724M1
APPLICANT: Ashbrook, Brian A.
APPLICANT: Friedrich, Glenn A.
APPLICANT: Ellender, Sean
APPLICANT: Ashbrook, Brian A.
TITLE OF INVENTION: VECTORS FOR GENE MUTAGENESIS AND GENE
DISCOVERY
CURRENT APPLICATION NUMBER: US/010/158,735
CURRENT FILING DATE: 2002-05-29
PRIOR FILING DATE: 1999-01-05, 09/26/533
PRIOR APPLICATION NUMBER: US 60/079,729
PRIOR FILING DATE: 1998-01-27, 6/0/081,727
PRIOR FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: US 60/109,302
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 25
TTSE: DNA
ORGANISM: Mus musculus
US-10-158-735-10
Query Match
Best Local Similarity 17.0% Score 15.8; DB 9; Length 35;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
DB      33  66066666CCTCCAGAACATCCAGG616 7

RESULT 8
US-10-043-573-45/C

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Query Match      17.0%  Score 15.8  DB 9  length 25
Best Local Similarity 89.5%  Pred. No. 1.2e+04
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

0y      66 TGTGGAGCGTCGACGAAGC 84
        |||||  |||||  |||||  ||
Db       2 TGTGGAGCTCCGACGAAGC 20

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RESULT 8

IS-10-043-573-45/c

Wf	67	0109060CCLCHSNDNCHL18M6B16	5
Dd	33	G6G6GTCTGGAGGCACATGAGGGr6	7

07 13 CCGCATCTGCTGGTGGGACAGACGCTCTGG 36
 11 11 11 11 11 11 11 11 11 11
 22 CCGCATCTGCTGGTGGGACAGACGCTCTGG 1

RESULT 12
 US-09-872-695A-40

? Sequence 40: Application US/09/75696A
 ? GENERAL INFORMATION: 35101061A1
 ? APPLICANT: JOHNSON, Julie C.
 ? APPLICANT: Sauter, Spillie L.
 ? APPLICANT: Sheridan, Phillip Lee
 ? APPLICANT: Hardy, Steven
 ? APPLICANT: Dubensky, Thomas
 ? APPLICANT: Resnick, William
 ? TITLE OF INVENTION: FEELING IMMUNODEFICIENCY VIRUS GENE THERAPY VECTORS
 ? FILE REFERENCE: 910049.467 US/09/797.518A
 ? CURRENT APPLICATION NUMBER: US/09/797.518A
 ? PRIOR APPLICATION NUMBER: 09/231.235
 ? PRIORITY FILING DATE: 1999-01-15
 ? NUMBER OF SEQ ID NOS: 63
 ? SEQ ID NO 40
 ? SOFTWARE: Paterlin Ver. 2.0
 ? LENGTH: 46
 ? ORGANISM: Artificial Sequence
 ? FEATURE: Artificial Sequence
 ? OTHER INFORMATION: Description of Artificial Sequence: Primer
 ? OTHER INFORMATION: Primer Used in Examples 3C and 5D
 US-09-872-695A-40

Query Match 15.3%; Score 15.2; DB 9; Length 46;
 Best Local Similarity 66.7%; Pred. No. 2, 6e+04;
 Matches 20; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
 07 13 CCGCATCTGCTGGTGGGACAGACGCTCTGG 42
 11 11 11 11 11 11 11 11 11 11
 22 CCGCATCTGCTGGTGGGACAGACGCTCTGG 42

RESULT 13
 US-09-211-235-40

? Sequence 40: Application US/09/31235
 ? Patent No. US2002004809A1
 ? APPLICANT: JOHNSON, Julie C.
 ? APPLICANT: Sauter, Spillie L.
 ? APPLICANT: Resnick, William
 ? APPLICANT: Hardy, Steven
 ? APPLICANT: Dubensky, Thomas
 ? APPLICANT: Resnick, William
 ? TITLE OF INVENTION: FEELING IMMUNODEFICIENCY VIRUS GENE THERAPY VECTORS
 ? FILE REFERENCE: 910049.467 US/09/797.518A
 ? CURRENT APPLICATION NUMBER: US/09/797.518A
 ? PRIOR APPLICATION NUMBER: 09/231.235
 ? PRIORITY FILING DATE: 1999-01-15
 ? NUMBER OF SEQ ID NOS: 63
 ? SEQ ID NO 40
 ? SOFTWARE: Paterlin Ver. 2.0
 ? LENGTH: 46
 ? ORGANISM: Artificial Sequence
 ? FEATURE: Artificial Sequence
 ? OTHER INFORMATION: Description of Artificial Sequence: Primer
 ? OTHER INFORMATION: Primer Used in Examples 3C and 5D
 US-09-211-235-40

Query Match 15.3%; Score 15.2; DB 10; Length 46;
 Best Local Similarity 66.7%; Pred. No. 2, 6e+04;
 Matches 20; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

07 13 CCGCATCTGCTGGTGGGACAGACGCTCTGG 42
 11 11 11 11 11 11 11 11 11 11
 22 CCGCATCTGCTGGTGGGACAGACGCTCTGG 42

RESULT 14
 US-09-797-518A-40

? Sequence 40: Application US/09/797518A
 ? Patent No. US0102008354A1
 ? APPLICANT: JOHNSON, Julie C.
 ? APPLICANT: Sauter, Spillie L.
 ? APPLICANT: Resnick, William
 ? APPLICANT: Hardy, Steven
 ? APPLICANT: Dubensky, Thomas
 ? APPLICANT: Resnick, William
 ? TITLE OF INVENTION: FEELING IMMUNODEFICIENCY VIRUS GENE THERAPY VECTORS
 ? FILE REFERENCE: 910049.467
 ? CURRENT APPLICATION NUMBER: US/09/797.518A
 ? PRIOR APPLICATION NUMBER: 09/231.235
 ? PRIORITY FILING DATE: 1999-01-15
 ? NUMBER OF SEQ ID NOS: 63
 ? SEQ ID NO 40
 ? SOFTWARE: Paterlin Ver. 2.0
 ? LENGTH: 46
 ? ORGANISM: Artificial Sequence
 ? FEATURE: Artificial Sequence
 ? OTHER INFORMATION: Description of Artificial Sequence: Primer
 ? OTHER INFORMATION: Primer Used in Examples 3C and 5D
 US-09-797-518A-40

Query Match 15.3%; Score 15.2; DB 10; Length 46;
 Best Local Similarity 66.7%; Pred. No. 2, 6e+04;
 Matches 20; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
 07 13 CCGCATCTGCTGGTGGGACAGACGCTCTGG 42
 11 11 11 11 11 11 11 11 11 11
 22 CCGCATCTGCTGGTGGGACAGACGCTCTGG 42

RESULT 15
 US-09-935-280-15

? Sequence 15: Application US/09/35280
 ? Patent No. US200003022179A1
 ? GENERAL INFORMATION: 35101061A1
 ? APPLICANT: INVITROGEN CORPORATION
 ? APPLICANT: CHRISTIAN, John
 ? APPLICANT: BRYMAN, John
 ? APPLICANT: MADDEN, Kate
 ? APPLICANT: Dubensky, Thomas
 ? APPLICANT: Resnick, William
 ? TITLE OF INVENTION: METHODS AND REAGENTS FOR MOLECULAR CLONING
 ? FILE REFERENCE: INVIT100-1-92/09/935.280
 ? CURRENT APPLICATION NUMBER: US/09/935.280
 ? PRIOR APPLICATION NUMBER: 09/231.235
 ? PRIORITY FILING DATE: 2000-08-21
 ? NUMBER OF SEQ ID NOS: 3
 ? SEQ ID NO 15
 ? SOFTWARE: Paterlin version 3.0
 ? LENGTH: 15
 ? ORGANISM: Artificial Sequence
 ? FEATURE: Artificial Sequence
 ? OTHER INFORMATION: Annealing oligonucleotide
 US-09-935-280-15

Query Match 15.1%; Score 15; DB 9; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2, 2e+04;


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DB      10 ATCTTCGACAAACACTTACCTACCTACCTAC 43
RESULT 36
US-10-215-112-842
/ Sequence 842, Application US/10215112
/ Best Local Similarity 81.0%, Pred. No. 3,6e+04
/ GENERAL INFORMATION:
/ APPLICANT: Michael Mitman
/ TITLE OF INVENTION: Probe Sequence Listing Generator V.1.1
/ FILE REFERENCE: 1119
/ CURRENT APPLICATION NUMBER: US/01215,112
/ PRIORITY APPLICATION NUMBER: US-08-08
/ NUMBER OF SEQ ID NOS: 14936
/ SOFTWARE: FASTEST for Windows version 4.0
/ SEQ ID NO: 14936
/ LENGTH: 25
/ TYPE: DNA
/ FEATURE: Artificial Sequence
/ OTHER INFORMATION: Synthetic oligonucleotide
US-10-215-112-842
Query Match      15.7%, Score 14.6; DB 9; Length 25;
Best Local Similarity 81.0%, Pred. No. 3,6e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

DB      30 GACATGCCCTGGCTTGCACCA 30
US-10-098-263B-40831
RESULT 37
US-10-098-263B-40831
/ Sequence 40831, Application US/10098263B
/ Best Local Similarity 81.0%, Pred. No. 3,6e+04
/ GENERAL INFORMATION:
/ APPLICANT: Mitman, Michael
/ TITLE OF INVENTION: Human Microarray
/ FILE REFERENCE: 1119
/ CURRENT APPLICATION NUMBER: US/01098,263B
/ PRIORITY APPLICATION NUMBER: US-03-16,759
/ CURRENT FILING DATE: 2003-01-08
/ PRIOR FILING DATE: 2001-03-16
/ NUMBER OF SEQ ID NOS: 11066
/ SEQ ID NO: 40831
/ SOFTWARE: Word 97 (MS-DOS text format)
/ LENGTH: 25
/ TYPE: DNA
/ FEATURE: Homo sapien
/ OTHER INFORMATION:
/ APPLICANT: Mitman, Michael
/ TITLE OF INVENTION: Human Microarray
/ FILE REFERENCE: 1118.1
/ CURRENT APPLICATION NUMBER: US/01098,263B
/ CURRENT FILING DATE: 2003-01-08
US-10-098-263B-40831
Query Match      15.7%, Score 14.6; DB 9; Length 25;
Best Local Similarity 81.0%, Pred. No. 3,6e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

DB      24 CTTGGGACACATCCATCTGCTT 44
US-10-098-263B-40831
RESULT 38
US-10-098-263B-40831
/ Sequence 99102, Application US/10098263B
/ Best Local Similarity 81.0%, Pred. No. 3,6e+04
/ GENERAL INFORMATION:
/ APPLICANT: Mitman, Michael
/ TITLE OF INVENTION: Human Microarray
/ FILE REFERENCE: 1118.1
/ CURRENT APPLICATION NUMBER: US/01098,263B
/ CURRENT FILING DATE: 2003-01-08
US-10-098-263B-40831
Query Match      15.7%, Score 14.6; DB 9; Length 25;
Best Local Similarity 81.0%, Pred. No. 3,6e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

DB      19 TCTCCCTGGCTGGACATCCCT 39
US-10-098-263B-99102
Query Match      15.7%, Score 14.6; DB 9; Length 25;
Best Local Similarity 81.0%, Pred. No. 6,6e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

DB      22 TCTACCCCGATGCACAAACCT 3
US-10-098-263B-99102
RESULT 39
US-10-098-263B-99102
/ Sequence 99102, Application US/09861292
/ Best Local Similarity 81.0%, Pred. No. 2,0e+04
/ Patent No. US2002015900A1
/ GENERAL INFORMATION:
/ APPLICANT: David J.
/ APPLICANT: Prudent, James R.
/ APPLICANT: Sherfili, Christopher B.
/ APPLICANT: Sherfili, Jennifer K.
/ APPLICANT: Richard, Craig S.
/ APPLICANT: Jurecy, Simon
/ CURRENT APPLICATION NUMBER: US/09861,292
/ PRIORITY APPLICATION NUMBER: US 60/205,112
/ PRIOR FILING DATE: 2000-05-19
/ PRIOR APPLICATION NUMBER: US 60/240,398
/ PRIOR FILING DATE: 2001-10-07
/ PRIOR APPLICATION NUMBER: US 60/282,931
/ PRIOR FILING DATE: 2001-04-10
/ SOFTWARE: Word 97 (MS-DOS text format)
/ SEQ ID NO: 37
/ TYPE: DNA
/ FEATURE: Homo sapien
/ OTHER INFORMATION:
/ APPLICANT: Basic Feature
/ NAME/KEY: modified base
/ NAME/KEY: modified base
/ OTHER INFORMATION: n represents deoxy-iso-cytosine (d-isoC)
/ NAME/KEY: modified base
/ OTHER INFORMATION: n represents deoxy-iso-cytosine (d-isoC)
/ OTHER INFORMATION: n represents deoxy-iso-cytosine (d-isoC)
US-09-861-292-37
Query Match      15.7%, Score 14.6; DB 10; Length 32;
Best Local Similarity 73.9%, Pred. No. 3,9e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

DB      24 CACGACATACATCCATCTGCTCT 26
US-09-861-292-37
RESULT 40
US-09-861-292-37
/ Sequence 855-30
/ Best Local Similarity 81.0%, Pred. No. 2,0e+04
/ Patent No. US2002011520A1
/ APPLICANT: Rondo, Reiji

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APPLICANT: MITRA, VITRA
 TITLE OF INVENTION: TEST STRIP AND METHOD OF PRODUCING PROTEINS USING THE
 CURRENT APPLICATION NUMBER: US/09/098,855
 CURRENT FILING DATE: 2001-07-20
 PRIOR APPLICATION NUMBER: 09/242,690
 PRIOR FILING DATE: 1999-08-23
 PRIOR APPLICATION NUMBER: JC 8/241062
 PRIOR FILING DATE: 1996-08-23
 SOFTWARE: Patent In Ver. 2.1
 SEQ ID NO 30
 TYPE: DNA
 ORGANISM: Artificial Sequence
 OTHER INFORMATION: Description of Artificial Sequence: Primer
 US-09-809-855-30
 Query Match 15.7% Score 14.6; DB 10; Length 38;
 Best Local Similarity 81.0%; Pct: No. 4.2e+04;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Oy 4 CCGGACGACGTCATGTCGCC 24
 17 CAGCAGCAGTCATTAATGCGC 37
 DB
 RESULT 41
 US-09-912-679-80
 Sequence 13; Application US/1018196
 Publication No. US2003009877A1
 APPLICANT: ALSO NO. US2003009877A1
 TITLE OF INVENTION: METHOD OF CRYSTALLIZING POLYPEPTIDE
 CURRENT FILING DATE: 2000-05-24
 PRIOR APPLICATION NUMBER: US/10/181,985
 CURRENT FILING DATE: 2002-07-19
 PRIOR APPLICATION NUMBER: PCT/EP01/00571
 PRIOR FILING DATE: 1999-10-17
 NUMBER OF SEQ ID NOS: 14
 SOFTWARE: Patent In Ver. 3.1
 OTHER INFORMATION: Description of Artificial Sequence: Primer
 US-10-181-856-13
 Query Match 15.7% Score 14.6; DB 9; Length 40;
 Best Local Similarity 69.0%; Pct: No. 4.2e+04;
 Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 Oy 48 AACATATCCGACATGTCATGTCGCC 76
 12 AACATATCCGACATGTCATGTCGCC 40
 DB
 RESULT 42
 US-09-912-679-80
 Sequence 80; Application US/09912679
 Patent No. US200201917A1
 APPLICANT: JOLLY, Douglas J.
 Chang, Stephen M.M.
 Townsend, Kay
 O'Dea, Jeanne
 TITLE OF INVENTION: HEPATITIS THERAPEUTICS
 NUMBER OF SEQ ID NOS: 100
 OTHER INFORMATION: o1190 55
 CORRESPONDENCE ADDRESS:

ADDRESSES: said and Betty
 STREET: 300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 ZIP: 98101-3
 COMPUTER READABLE FORM:
 OPERATING SYSTEM: PC-DOS/MS-DOS
 COMPUTER: IBM PC compatible
 CURRENT FILING DATE: 1999-10-02
 PRIOR APPLICATION NUMBER: US/09/912,679
 FILING DATE: 07-Jun-1995
 NAME: Knebelers, David D.
 ATTORNEY/AGENT INFORMATION:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206/452-9000
 TELEFAX: 206/452-6031
 TEXT: 372836
 INFORMATION FOR SEQ ID NO: 80:
 SUBSEQUENCE: 40 base pairs
 TYPE: nucleic acid
 LENGTH: 40 base pairs
 TOPOLOGY: linear
 US-09-912-679-80
 SEQUENCE DESCRIPTION: SEQ ID NO: 80:
 Query Match 15.7% Score 14.6; DB 10; Length 40;
 Best Local Similarity 81.0%; Pct: No. 4.2e+04;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Oy 72 GCTCTGCAACATGATGAT 92
 DB 13 GCTCTGCAACATGATGAT 33
 DB
 RESULT 43
 US-10-193-960-55/c
 Sequence 55; Application US/1019360
 Publication No. US20030104477A1
 APPLICANT: Buehler, Joe
 OTHER INFORMATION: Gray, Jeff; Gurnas
 TITLE OF INVENTION: Diagnostic Polyclonal Antibodies
 CURRENT FILING DATE: 2002-07-12
 PRIOR APPLICATION NUMBER: US/10/193,960
 CURRENT FILING DATE: 1999-10-02
 PRIOR APPLICATION NUMBER: US 08/832,985
 PRIOR FILING DATE: 1997-04-04
 PRIOR APPLICATION NUMBER: NO PCT/US96/6704
 PRIOR FILING DATE: 1996-08-23
 NUMBER OF SEQ ID NOS: 100
 SOFTWARE: FastSeq for Windows version 3.0
 LENGTH: 43
 TYPE: DNA
 ORGANISM: Artificial Sequence
 OTHER INFORMATION: o1190 55
 US-10-193-960-55
 Query Match 15.7% Score 14.6; DB 9; Length 43;


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/ SEQ ID NO 53
/ LENGTH: 45
/ TYPE: DNA
/ ORGANISM: Canis familiaris
/ NAME/TEXT: CDS (1..45)
/ ORIGIN:
US-09-818-063-53
Query Match
Beat Local Similarity 15.7%; Score 14.6; DB 10; Length 45;
Matches 26; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
DB 45 CTTGGACCTCTCGGCGACATGTCCTTCACAGACTTGGTTCCA 1

RESULT 53
US-09-996-073-19
/ Sequence 55, Application US/0991063
/ Patent No. US2002009856A1
/ APPLICANT: Robert R. Eric R.
/ APPLICANT: Jason, Wayne A.
/ APPLICANT: Chondrasekar, Ramaswamy
/ TITLE OF INVENTION: A METHOD FOR IDENTIFYING HIGH PROTEINS, NUCLEIC ACID MOLECULES, AND USING THEREOF
/ FILE REFERENCE: 02-12
/ CURRENT APPLICATION NUMBER: US/09/918, 063
/ PRIOR APPLICATION NUMBER: 60/224, 655
/ PRIOR FILING DATE: 2000-08-11
/ SOFTWARE: Patfield version 3.1
/ SEQ ID NO 55
/ LENGTH: 45
/ TYPE: DNA
/ ORGANISM: Canis familiaris
US-09-918-063-55
Query Match
Beat Local Similarity 15.7%; Score 14.6; DB 10; Length 45;
Matches 26; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
DB 4 CTTGGACCTCTCGGCGACATGTCCTTCACAGACTTGGTTCCA 48
1 CTTGGACCTCTCGGCGACATGTCCTTCACAGACTTGGTTCCA 45

RESULT 53
US-09-996-073-19
/ Sequence 19, Application US/0996073
/ Patent No. US2003000355A1
/ APPLICANT: JENSEN, JR., Thomas W.
/ APPLICANT: GINSKY, Melvin
/ TITLE OF INVENTION: FUNCTIONAL LENTIVIRAL VECTOR FROM
/ TITLE OF INVENTION: AN HIV-BASED BACULONE
/ CURRENT APPLICATION NUMBER: US/09/996, 073
/ PRIOR FILING DATE: 2001-11-27
/ SOFTWARE: SeqScribe Ver. 2.0
/ SEQ ID NO 19
/ LENGTH: 46
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ NAME/TEXT: Description of Artificial Sequence: HIV primer

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/ LOCATION: (29)
/ OTHER INFORMATION: "n" = "c" or "t"
US-09-996-073-19
Query Match
Beat Local Similarity 15.7%; Score 14.6; DB 9; Length 46;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
DB 13 CTTGACCTCTCGGCGACATGTCCTTCACAGACTTGGTTCCA 42
13 CTTGACCTCTCGGCGACATGTCCTTCACAGACTTGGTTCCA 42

RESULT 53
US-09-853-745-27/c
/ Sequence 27, Application US/0983745
/ Publication No. US2003003959A1
/ APPLICANT: Peng, Yu
/ APPLICANT: Peng, Yu
/ TITLE OF INVENTION: A METHOD FOR IDENTIFYING HIGH PROTEINS, NUCLEIC ACID MOLECULES, AND USING THEREOF
/ FILE REFERENCE: 12934-002001
/ CURRENT APPLICATION NUMBER: US/09/853, 745
/ PRIOR APPLICATION NUMBER: US 60/286, 997
/ PRIOR FILING DATE: 2000-05-24
/ SOFTWARE: Patfield for Windows version 4.0
/ SEQ ID NO 27
/ LENGTH: 46
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ OTHER INFORMATION: synthetically generated primer
US-09-853-745-27
Query Match
Beat Local Similarity 15.7%; Score 14.6; DB 9; Length 46;
Matches 23; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
DB 16 CATTTCCTCTCGGCGACATGTCCTTCACAGACTTGGTTCCA 52
48 CATTTCCTCTCGGCGACATGTCCTTCACAGACTTGGTTCCA 52

RESULT 54
US-09-996-073-19
/ Sequence 115, Application US/0963806
/ Publication No. US2002019760A1
/ APPLICANT: JENSEN, JR., Thomas W.
/ APPLICANT: GINSKY, Melvin
/ TITLE OF INVENTION: DETECTION OF MICROPLASMA BY ANALYSIS OF SALIVA
/ NUMBER OF SEQUENCES: 195
/ ADDRESS: Fish & Richardson P.C.
/ STREET: 4225 Executive Square, Suite 1400
/ CITY: CA, Dallas
/ STATE: TX, USA
/ COUNTRY: USA
/ FILING DATE: 2001-11-27
/ COMPILED BY: David
/ COMPUTER: IBM compatible
/ SOFTWARE: PASTSEQ for Windows Version 2.0b
/ CURRENT APPLICATION DATA:
/ FILING DATE: 22-May-2001
/ APPLICATION NUMBER: 09/098, 637
/ APPLICATION NUMBER: 08/552, 313

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US-09-829-124-5
Query Match 15.3% Score 14.2; DB 9; Length 33;
Best Local Similarity 70.4% Pred. No. 6,4e+04;
Matches 13; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

DB 20 CACTGCGGAGTACGCTCGGTTG 46
30 CACTGCGGAGTACGCTCGGTTG 46

RESULT 78
US-10-043-573-131
Sequence 517; Application US/0043573
GENERAL INFORMATION:
APPLICANT: Lambeau, Richard
TITLE OF INVENTION: Bacterial Polymorphisms
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
ATTORNEY/AGENT INFORMATION:
FILING DATE: 09-Jan-2002
PRIORITY APPLICATION DATA: US/10/043,573
CURRENT APPLICATION DATA: US/10/043,573
SOFTWARE: PUBLISHED FOR Windows Version 2.0
CLASSIFICATION: <UNKNOWN>
PRIORITY APPLICATION NUMBER: US/08/813,507
FILING DATE: 07-MAR-1997
PRIORITY FILING DATE: 02-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lachapin, J. J.
REFERENCE/DOCKET NUMBER: 019547-03010008
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415 576-0200
TELEFAX: 415 576-0200
TEXT: <UNKNOWN>
INFORMATION:
SEQUENCE IDENTIFICATION:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
LENGTH: 42 base pairs
SOURCE: Human
SOFTWARE: Pileup version 3.1
US-10-043-573-131
SEQUENCE DESCRIPTION: SEQ ID NO: 131:
Query Match 15.3% Score 14.2; DB 9; Length 42;
Best Local Similarity 85.9% Pred. No. 6,4e+04;
Matches 13; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

DB 42 GATGACATGTCGAGTGTGATGCTG 70
4 GATGACATGTCGAGTGTGATGCTG 72

RESULT 79
US-08-781-986A-2061/C
Sequence 661; Application US/08/81986A
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION:
CORRESPONDENCE ADDRESS:
ADDRESS:
ATTORNEY/AGENT INFORMATION:
FILING DATE:
PRIORITY APPLICATION DATA:
CURRENT APPLICATION DATA:
SOFTWARE:
CLASSIFICATION:
PRIORITY APPLICATION NUMBER:
FILING DATE:
PRIORITY FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME:
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX:
TEXT:
INFORMATION:
SEQUENCE IDENTIFICATION:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
LENGTH: 50 base pairs
SOURCE: Human
SOFTWARE: Pileup version 3.1
US-08-781-986A-2061/C
SEQUENCE DESCRIPTION:
Query Match 15.3% Score 14.2; DB 7; Length 50;
Best Local Similarity 84.2% Pred. No. 6,4e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

DB 27 GATGACATGTCGAGTGTG 45
41 GATGACATGTCGAGTGTG 43

RESULT 80
US-09-940-185-517/C
Sequence 517; Application US/09/0185
GENERAL INFORMATION:
APPLICANT: Genderson, Kevin
TITLE OF INVENTION: Probe and Decipher Oligonucleotides
CORRESPONDENCE ADDRESS:
ADDRESS:
ATTORNEY/AGENT INFORMATION:
FILING DATE:
PRIORITY APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/09/940,185
FILING DATE: 2001-08-27/227,348
PRIORITY FILING DATE: 2000-08-25/60,227,348
PRIORITY APPLICATION NUMBER: US 60/228,354
PRIORITY FILING DATE: 2000-08-25/60,228,354
NUMBER OF SEQ ID NOS: 4768
SOURCE: Human
SOFTWARE: Pileup version 3.1
US-09-940-185-517
SEQUENCE DESCRIPTION:
Query Match 15.3% Score 14; DB 9; Length 24;
Best Local Similarity 77.3% Pred. No. 6,4e+04;

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Matches 17: Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 18 TTCCTCGGATCGATTCACAAACCT 39
Db 23 TTTCTCGGATCGATTCACAAACCT 2

RESULT 81
US-09-340-185-1258
Sequence 1258, Application US/09340185
GENERAL INFORMATION:
APPLICANT: Guiderson, Kevin
FILE REFERENCE: A-69605-1
CURRENT APPLICATION NUMBER: US/09340185
PRIOR APPLICATION NUMBER: US 60/227,948
PRIOR FILING DATE: 2000-08-25
PRIOR FILING DATE: 2000-08-25
NUMBER OF SEQ ID NOS: 4768
SD ID NO 4468
SEQUENCE VERSION: 3.1
LENGTH: 24
TYPE: DNA
FEATURE: Artificial Sequence
OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-340-185-1258

Query Match 15.1% Score 14; Db 9; Length 25;
Best Local Similarity 77.3% Pred. No. 6.2e+04;
Matches 17: Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 66 TGTGTGCGGATTCGATTCACAAACCT 87
Db 3 TTTCTCGGATCGATTCACAAACCT 24

RESULT 82
US-10-215-112-919/c
Sequence 919, Application US/0215112
GENERAL INFORMATION:
APPLICANT: Michael Mittman
FILE REFERENCE: Tect3
CURRENT APPLICATION NUMBER: US/10/215,112
PRIOR APPLICATION NUMBER: US 60/227,948
NUMBER OF SEQ ID NOS: 14936
SOFTWARE: PARSED for Windows version 4.0
SD ID NO 4468
SEQUENCE VERSION: 3.1
LENGTH: 23
TYPE: DNA
FEATURE: Artificial Sequence
OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-919

Query Match 15.1% Score 14; Db 9; Length 25;
Best Local Similarity 77.3% Pred. No. 6.2e+04;
Matches 17: Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 30 GAAATTCGATTCGATTCACAAAC 51
Db 22 GGTATTCGATTCGATTCACAAAC 1

RESULT 83
US-09-340-185-1258
Sequence 1258, Application US/09340185
GENERAL INFORMATION:
APPLICANT: Guiderson, Kevin
FILE REFERENCE: A-69605-1
CURRENT APPLICATION NUMBER: US/09340185
PRIOR APPLICATION NUMBER: US 60/227,948
PRIOR FILING DATE: 2000-08-25
PRIOR FILING DATE: 2000-08-25
NUMBER OF SEQ ID NOS: 4768
SD ID NO 4468
SEQUENCE VERSION: 3.1
LENGTH: 24
TYPE: DNA
FEATURE: Artificial Sequence
OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-340-185-1258

Query Match 15.1% Score 14; Db 9; Length 25;
Best Local Similarity 77.3% Pred. No. 6.2e+04;
Matches 17: Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 66 TGTGTGCGGATTCGATTCACAAACCT 87
Db 3 TTTCTCGGATTCGATTCACAAACCT 24

RESULT 84
US-09-340-185-1258/c
Sequence 1258, Application US/09340185
GENERAL INFORMATION:
APPLICANT: Guiderson, Kevin
FILE REFERENCE: A-69605-1
CURRENT APPLICATION NUMBER: US/09340185
PRIOR APPLICATION NUMBER: US 60/227,948
PRIOR FILING DATE: 2000-08-25
PRIOR FILING DATE: 2000-08-25
NUMBER OF SEQ ID NOS: 4768
SD ID NO 4468
SEQUENCE VERSION: 3.1
LENGTH: 24
TYPE: DNA
FEATURE: Artificial Sequence
OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-340-185-1258

Query Match 15.1% Score 14; Db 9; Length 25;
Best Local Similarity 77.3% Pred. No. 6.2e+04;
Matches 17: Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 30 GAAATTCGATTCGATTCACAAAC 51
Db 4 GGTATTCGATTCGATTCACAAAC 25

RESULT 85
US-10-098-2638-62496
Sequence 62496, Application US/100982638
GENERAL INFORMATION:
APPLICANT: Mittman, Michael
FILE REFERENCE: Tect3
CURRENT APPLICATION NUMBER: US/10/098,2638
PRIOR APPLICATION NUMBER: US 60/227,948
NUMBER OF SEQ ID NOS: 14936
SOFTWARE: PARSED for Windows version 4.0
SD ID NO 4468
SEQUENCE VERSION: 3.1
LENGTH: 23
TYPE: DNA
FEATURE: Artificial Sequence
OTHER INFORMATION: Synthetic Oligonucleotide
US-10-098-2638-62496

Query Match 15.1% Score 14; Db 9; Length 25;
Best Local Similarity 77.3% Pred. No. 6.2e+04;
Matches 17: Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 18 TTCCTCGGATTCGATTCACAAACCT 39
Db 24 TTTCTCGGATTCGATTCACAAACCT 3

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1 FILE REFERENCE: 2825, 2011-01-001
2
3 CURRENT APPLICATION NUMBER: US/09/912,263
4
5 CURRENT FILING DATE: 2001-07-24
6
7 PRIOR APPLICATION NUMBER: US 60/220,315
8
9 PRIOR FILING DATE: 2000-07-24
10
11 NUMBER OF SEQ ID NOS: 552
12
13 SOFTWARE: FASTEST for Windows Version 4.0.
14
15 SEQ ID NO 506
16
17 LENGTH: 31
18
19 TYPE: DNA
20
21 ORGANISM: Homo sapiens
22
23 US 09/912,263-506

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Query Match      13.1%; Score 14; DB 9; Length 31;
Best Local Similarity 70.8%; Pred. No. 6.6e+04;
Matches 17; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

      13 CCGCATTCGCGCGGACAGC 36
      ||| ||||| ||||| ||| |||
Db      2 CTAATATCCCGCATTCGCGCATTC 25

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1 SHD ID NO 103
2 SHD ID NO 103
3 TYPE: DNA
4 ORGANISM: Artificial Sequence
5 FEATURE:
6 OTHER INFORMATION: Primer R0720
7 US-95-03_455-103
8
9 Query Match
10 Best Local Similarity 15.14; Score 14; DB 10; Length 30;
11 Matches 20; Conservative 0; Mismatches 10;
12
13 27 GGTGGACAGCCGTCGATTCACACATGAC 56
14
15 DB 1 GGTTCGACAGCCGTCGATTCACACATGAC 30
16
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18 RESULT 32
19 US-95-03_263-506
20 Publication 506; Application US/0991263
21
22 GENERAL INFORMATION:
23 Title: Single-strand DNA molecule
24 Applicant: Ireland, James S.
25 Applicant: Ireland, James S.
26 Title of Invention: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS

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06-10-02-29-314-21
07 OTHER INFORMATION: Description of Artificial Sequence: plasmid/probe
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APPLICANT: Lander, Eric S.
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS

```

/ SEQ ID NO 21
/ LENGTH: 32
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ OTHER INFORMATION: Description of Artificial Sequence: primer/probe
US-10-023-314-21

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Query Match      15.1% Score 14; DB 9; Length 32;
Best Local Similarity 66.7% Pred. No. 6.7e+04;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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DB 3 CACCTCCCTTCCTCCGGGTGCACACACCTT 40

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RESULT 95
US-09-899-732-20/C
/ Sequence 20: Application US/09899732
/ Patent No. US6200111306A1
/ GENERAL INFORMATION:
/ APPLICANT: Salton et al, John A.
/ TITLE OF INVENTION: A Human Melanin Concentrating Hormone
/ FILE REFERENCE: 1795/57453-C/JP
/ CURRENT FILING DATE: 2001-09-24
/ PRIOR APPLICATION NUMBER: 09/6510,635
/ PRIOR FILING DATE: 2000-07-05
/ NUMBER OF SEQ IDS: 28
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 20
/ LENGTH: 32
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ OTHER INFORMATION: Description of Artificial Sequence: primer/probe
US-09-899-732-20

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Query Match      15.1% Score 14; DB 9; Length 32;
Best Local Similarity 66.7% Pred. No. 6.7e+04;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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DB 11 CACCTCCCTTCCTCCGGGTGCACACACCTT 40

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DB 30 CACCTCCCTTCCTCCGGGTGCACACACCTT 1

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RESULT 96

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US-09-899-732-21
/ Sequence 21: Application US/09899732
/ Patent No. US6200111306A1
/ GENERAL INFORMATION:
/ APPLICANT: Salton et al, John A.
/ TITLE OF INVENTION: DNA Encoding a Human Melanin Concentrating Hormone
/ FILE REFERENCE: 1795/57453-C/JP
/ CURRENT FILING DATE: 2001-09-24
/ PRIOR APPLICATION NUMBER: 09/6510,635
/ PRIOR FILING DATE: 2000-07-05
/ NUMBER OF SEQ IDS: 28
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 21
/ LENGTH: 32
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: primer/probe
US-09-899-732-21

```

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Query Match      15.1% Score 14; DB 9; Length 32;

```

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Best Local Similarity 66.7% Pred. No. 6.7e+04;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

```

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DB 11 CACCTCCCTTCCTCCGGGTGCACACACCTT 40

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DB 3 CACCTCCCTTCCTCCGGGTGCACACACCTT 32

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RESULT 97
US-09-899-478-20/C
/ Sequence 20: Application US/09899478
/ Patent No. US6200111306A1
/ GENERAL INFORMATION:
/ APPLICANT: Salton, Thomas M
/ TITLE OF INVENTION:
/ FILE REFERENCE: 1795/57453-A-PT-US
/ CURRENT FILING DATE: 2001-09-24
/ PRIOR APPLICATION NUMBER: PCY/US97/31169
/ NUMBER OF SEQ IDS: 28
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 20
/ LENGTH: 32
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ OTHER INFORMATION: PRIMER
US-09-899-478-20

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Query Match      15.1% Score 14; DB 10; Length 32;
Best Local Similarity 66.7% Pred. No. 6.7e+04;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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DB 11 CACCTCCCTTCCTCCGGGTGCACACACCTT 40

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DB 30 CACCTCCCTTCCTCCGGGTGCACACACCTT 1

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RESULT 98

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US-09-899-478-21
/ Sequence 21: Application US/09899478
/ Patent No. US6200111306A1
/ GENERAL INFORMATION:
/ APPLICANT: Salton, John A
/ TITLE OF INVENTION: DNA Encoding a Human Melanin Concentrating Hormone Receptor (M
/ FILE REFERENCE: 1795/57453-A-PT-US
/ CURRENT FILING DATE: 2001-09-24
/ PRIOR APPLICATION NUMBER: 09/6510,635
/ PRIOR FILING DATE: 1999-11-30
/ NUMBER OF SEQ IDS: 28
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 21
/ LENGTH: 32
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE: PRIMER
/ OTHER INFORMATION: PRIMER
US-09-899-478-21

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Query Match      15.1% Score 14; DB 10; Length 32;
Best Local Similarity 66.7% Pred. No. 6.7e+04;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Job time : 123 secs

07 11 CACTCCATCTCCCTCCCTCCCTCCCTCCCT 40
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 ID 3 CACTCCATCTCCCTCCCTCCCTCCCTCCCT 32

Result 99 US-102-948-2/C

Sequence 2: Alignment US/0102948
 Patent No. US20020197140A1

GENERAL INFORMATION:

INVENTOR: Chua, Nam-hai

APPLICANT: Chua, Nam-hai

TITLE OF INVENTION: EST - A PLANT GENE THAT CAN PROMOTE PLANT REGENERATION

FILE REFERENCE: 23-10-2-1

CURRENT FILING DATE: 2002-03-22

PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 13

SEQ ID NO: 2

LENGTH: 34

FEATURE: Artificial Sequence

OTHER INFORMATION: Description of Artificial Sequence: Second strand

US-102-948-2

Query Match

Best Local Similarity 15.1% Score 14; DB 9; Length 34;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

07 10 GACTCCATCTCCCTCCCTCCCTCCCTCCCT 39
 ||||| ||||| ||||| ||||| ||||| |||||

ID 30 GCTCCCATCTCCCTCCCTCCCTCCCTCCCT 1

Result 100 US-102-948-2/C

Sequence 1456: Alignment US/1000956

Publication No. US2003011726A1

GENERAL INFORMATION:

INVENTOR: Chua, Nam-hai

APPLICANT: Chua, Nam-hai

TITLE OF INVENTION: HUMAN SINGLE STRAND POLYMORPHISMS

FILE REFERENCE: D0053MP

CURRENT APPLICATION NUMBER: US/01005, 956

PRIOR APPLICATION NUMBER: 60/251, 015

PRIOR FILING DATE: 2000-12-04

PRIOR FILING DATE: 2001-01-23

PRIOR FILING DATE: 2001-01-23

PRIOR FILING DATE: 2001-01-23

NUMBER OF SEQ ID NOS: 1579

SOFTWARE: Patent version 3.0

SEQ ID NO: 135

LENGTH: 34

FEATURE: Artificial Sequence

OTHER INFORMATION: Description of Artificial Sequence: Second strand

US-102-948-2

Query Match

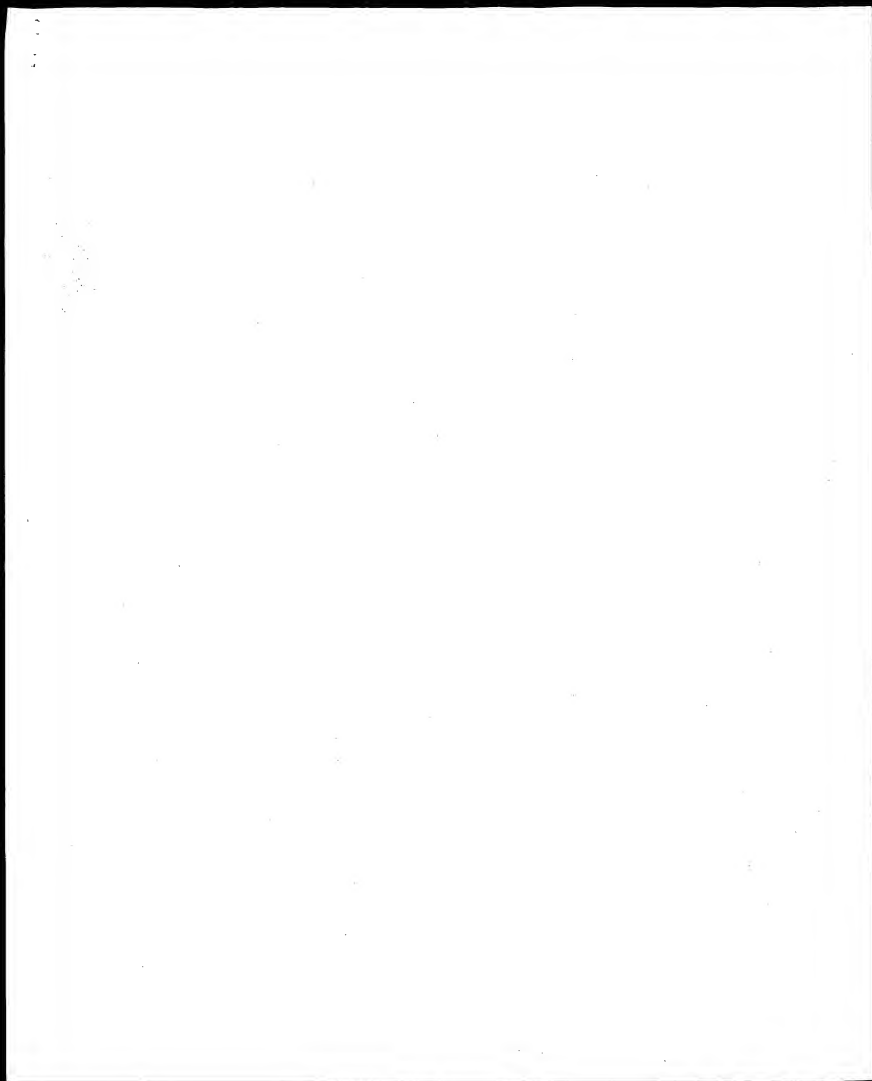
Best Local Similarity 15.1% Score 14; DB 9; Length 39;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

07 18 TTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 47
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ID 32 TTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3

Search completed: July 5, 2003, 13:11:58



685	12.6	13.5	42.2	US-08-973-124-778	Sequence 218, App	C 158	12.4	13.3	26.4	US-09-613-928-146	Sequence 146, App
686	13.1	13.5	42.2	US-08-973-124-780	Sequence 280, App	C 159	12.4	13.3	27.1	US-07-807-928-142	Sequence 42, App
687	13.1	13.5	42.2	US-08-973-124-782	Sequence 280, App	C 160	12.4	13.3	27.1	US-07-807-928-142	Sequence 42, App
688	12.6	13.5	42.2	US-08-973-124-784	Sequence 21, App	C 161	12.4	13.3	27.1	US-08-431-924-113	Sequence 113, App
689	12.6	13.5	42.2	US-08-973-124-786	Sequence 21, App	C 162	12.4	13.3	27.1	US-08-431-924-113	Sequence 113, App
690	12.6	13.5	42.2	US-08-973-124-788	Sequence 21, App	C 163	12.4	13.3	27.1	US-08-431-924-113	Sequence 113, App
691	12.6	13.5	42.2	US-08-973-124-790	Sequence 21, App	C 164	12.4	13.3	27.1	US-08-431-924-113	Sequence 113, App
692	12.6	13.5	42.2	US-08-973-124-792	Sequence 21, App	C 165	12.4	13.3	27.1	US-08-431-924-113	Sequence 113, App
693	12.6	13.5	42.2	US-08-973-124-794	Sequence 21, App	C 166	12.4	13.3	27.1	US-08-431-924-113	Sequence 113, App
694	12.6	13.5	42.2	US-08-973-124-796	Sequence 21, App	C 167	12.4	13.3	27.1	US-08-431-924-113	Sequence 113, App
695	12.6	13.5	42.2	US-08-973-124-798	Sequence 21, App	C 168	12.4	13.3	27.1	US-08-431-924-113	Sequence 113, App
696	12.6	13.5	42.2	US-08-973-124-800	Sequence 21, App	C 169	12.4	13.3	27.1	US-08-431-924-113	Sequence 113, App
697	12.6	13.5	42.2	US-08-973-124-802	Sequence 21, App	C 170	12.4	13.3	27.1	US-08-431-924-113	Sequence 113, App
698	12.6	13.5	42.2	US-08-973-124-804	Sequence 21, App	C 171	12.4	13.3	27.1	US-08-431-924-113	Sequence 113, App
699	12.6	13.5	42.2	US-08-973-124-806	Sequence 21, App	C 172	12.4	13.3	27.1	US-08-431-924-113	Sequence 113, App
700	12.6	13.5	42.2	US-08-973-124-808	Sequence 21, App	C 173	12.4	13.3	27.1	US-08-431-924-113	Sequence 113, App
701	12.6	13.5	42.2	US-08-973-124-810	Sequence 21, App	C 174	12.4	13.3	27.1	US-08-431-924-113	Sequence 113, App
702	12.6	13.5	42.2	US-08-973-124-812	Sequence 21, App	C 175	12.4	13.3	27.1	US-08-431-924-113	Sequence 113, App
703	12.6	13.5	42.2	US-08-973-124-814	Sequence 21, App	C 176	12.4	13.3	27.1	US-08-431-924-113	Sequence 113, App
704	12.6	13.5	42.2	US-08-973-124-816	Sequence 21, App	C 177	12.4	13.3	27.1	US-08-431-924-113	Sequence 113, App
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706	12.6	13.5	42.2	US-08-973-124-820	Sequence 21, App	C 179	12.4	13.3	27.1	US-08-431-924-113	Sequence 113, App
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708	12.6	13.5	42.2	US-08-973-124-824	Sequence 21, App	C 181	12.4	13.3	27.1	US-08-431-924-113	Sequence 113, App
709	12.6	13.5	42.2	US-08-973-124-826	Sequence 21, App	C 182	12.4	13.3	27.1	US-08-431-924-113	Sequence 113, App
710	12.6	13.5	42.2	US-08-973-124-828	Sequence 21, App	C 183	12.4	13.3	27.1	US-08-431-924-113	Sequence 113, App
711	12.6	13.5	42.2	US-08-973-124-830	Sequence 21, App	C 184	12.4	13.3	27.1	US-08-431-924-113	Sequence 113, App
712	12.6	13.5	42.2	US-08-973-124-832	Sequence 21, App	C 185	12.4	13.3	27.1	US-08-431-924-113	Sequence 113, App
713	12.6	13.5	42.2	US-08-973-124-834	Sequence 21, App	C 186	12.4	13.3	27.1	US-08-431-924-113	Sequence 113, App

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c 979 13.2 13.1 20 4 US-09-658-4837-47 Sequence 49, Appl
c 980 13.2 13.1 21 1 US-08-030-743-27 Sequence 2, Appl
c 981 13.2 13.1 21 1 US-08-030-743-27 Sequence 3, Appl
c 982 13.2 13.1 21 1 US-08-437-648-77 Sequence 7, Appl
c 983 13.2 13.1 21 1 US-08-437-648-77 Sequence 8, Appl
c 984 13.2 13.1 22 1 US-08-437-648-77 Sequence 9, Appl
c 985 13.2 13.1 22 1 US-08-437-648-77 Sequence 10, Appl
c 986 13.2 13.1 22 2 US-08-437-648-77 Sequence 11, Appl
c 987 13.2 13.1 22 2 US-08-437-648-77 Sequence 12, Appl
c 988 13.2 13.1 22 4 US-08-437-648-77 Sequence 13, Appl
c 989 13.2 13.1 22 4 US-08-437-648-77 Sequence 14, Appl
c 990 13.2 13.1 22 4 US-08-437-648-77 Sequence 15, Appl
c 991 13.2 13.1 22 4 US-08-437-648-77 Sequence 16, Appl
c 992 13.2 13.1 23 1 US-08-217-528-18-2 Sequence 18, Appl
c 993 13.2 13.1 24 1 US-08-217-528-18-2 Sequence 19, Appl
c 994 13.2 13.1 24 2 US-08-217-528-18-2 Sequence 20, Appl
c 995 13.2 13.1 24 2 US-08-217-528-18-2 Sequence 21, Appl
c 996 13.2 13.1 25 2 US-08-655-445-9 Sequence 4, Appl
c 997 13.2 13.1 25 2 US-08-655-445-9 Sequence 5, Appl
c 998 13.2 13.1 25 2 US-08-655-445-9 Sequence 6, Appl
c 999 13.2 13.1 25 4 US-09-381-259-8 Sequence 8, Appl
c1000 13.2 13.1 25 4 US-09-645-370-8 Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-08-602-716-8
Sequence 8 Application US/0802716A
Patent No. 5962664
GENERAL INFORMATION:
INVENTOR: ROBERT H. FITCHAM, Daryl A.
APPLICANT: BISHAM, Daryl A.
TITLE OF INVENTION: TRANSDUCER FOR DETECTING NUCLEAR ACID
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS: 12
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004
COMPUTER: IBM PC compatible
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC DOS/MS-DOS
SEQUENCE CHARACTERISTICS:
CURRENT APPLICATION DATA: Version #1.10
APPLICATION NUMBER: US/08/602,716A
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
FILING DATA: US-09/060,560
PRIOR APPLICATION DATA: US-09/060,560
APPLICATION NUMBER: US-09/060,560
FILING DATA: US-09/060,560
APPLICATION NUMBER: US-09/060,560
FILING DATA: US-09/060,560
ATTORNEY/AGENT INFORMATION:
NAME: BISHAM, ROBERT H.
REFERENCE/DOCKET NUMBER: FITCHAM-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-5297
TELEFAX: 202/371-5297
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid

STRANDNESS: single
MOLECULE TYPE: CNA
US-08-602-716-8
Query Match 20 (8) Score 18 6; DB 2 Length 45;
Best Local Similarity 84 (8); Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
DB 4 GCGCTCCCTGCTCCGCGGCACTC 34
10 GCGCTCCCTGCTCCGCGGCACTC 28
RESULT 2
US-08-331-081B-14
Sequence 14 Application US/08331081B
GENERAL INFORMATION:
INVENTOR: Daryl H. Fitcham, Robert H.
APPLICANT: BISHAM, Robert H.
TITLE OF INVENTION: TRANSDUCER FOR DETECTING NUCLEAR ACID
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS: 12
STREET: 419 Seventh Street, Suite 300
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004
COMPUTER: IBM PC compatible
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC DOS 5.0
SEQUENCE CHARACTERISTICS:
CURRENT APPLICATION DATA: Version #1.10
APPLICATION NUMBER: US/08/331,081B
CLASSIFICATION: 435
PRIOR APPLICATION DATA: 2,118,138
APPLICATION NUMBER: US-08/331,081B
FILING DATA: US-08/331,081B
APPLICATION NUMBER: US-08/331,081B
FILING DATA: US-08/331,081B
ATTORNEY/AGENT INFORMATION:
NAME: FITCHAM, ROBERT H.
REFERENCE/DOCKET NUMBER: FITCHAM-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-5297
TELEFAX: 202/371-5297
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDNESS: single
US-08-331-081B-14
Query Match 17 (8) Score 16 6; DB 2 Length 20;
Best Local Similarity 82 (8); Pred. No. 6.4e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
DB 17 ATCCGCTCCGCGGCACTC 39
11 ATCCGCTCCGCGGCACTC 29
RESULT 3
US-08-324-317C
Sequence 31 Application US/08223224
Patent No. 5635399
GENERAL INFORMATION:
INVENTOR: ROBERT H. FITCHAM, Robert J.
APPLICANT: KEITHMAN, Robert J.


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1 TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND
2 PROTEIN BINDING DOMAINS
3 NUMBER OF SEQUENCES: 57
4 COMPLETION DATE: 08-APR-1994
5 ADDRESS: Townsend and Townsend Knorrie and Crew
6 STREET: Seagate Street, Tower, One Market Plaza
7 CITY: San Francisco
8 STATE: CA
9 COUNTRY: US
10
11 INT: 94100-149 PDB
12 COMPILED BY: PDB
13 MEDIUM TYPE: Floppy disk
14 SOFTWARE: PDB
15 CURRENT APPLICATION DATA: 08/09/225,224
16 PUBLICATION NUMBER: 08/09/225,224
17 CLASSIFICATION: 530
18 ATTORNEY/AGENT INFORMATION:
19 REGISTRATION NUMBER: 32,762
20 REFERENCE/DOCKET NUMBER: 15280-193
21 TELEPHONE: (415) 543-6600
22 TELEFAX: (415) 543-5043
23 INFORMATION FOR SEQ ID NO: 31:
24 LENGTH: 39 base pairs
25 TYPE: nucleic acid
26 TOPOLOGY: linear
27
28 MOLECULE TYPE: DNA (primer)
29
30 US-08-722-258-31
31
32 Query Match 17.8% Score 16.6; DB 1; Length 39;
33 Best Local Similarity 17.0%; Pred. No. 7,3e+02;
34 Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
35
36 43 TTCCACCTCCGAGATGATCTGCGCGC 73
37
38 DB 35 TCTCAGCTCCGAGATGATCTGCGCGC 5
39
40 RESULT 4
41 Sequence 31: Application US/0872258
42 GENERAL INFORMATION:
43 TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND
44 PROTEIN BINDING DOMAINS
45 NUMBER OF SEQUENCES: 57
46 COMPLETION DATE: 08-APR-1994
47 ADDRESS: Townsend and Townsend Knorrie and Crew
48 STREET: Seagate Street, Tower, One Market Plaza
49 CITY: San Francisco
50 STATE: CA
51 COUNTRY: US
52
53 INT: 94111-3934
54 COMPILED BY: PDB
55 MEDIUM TYPE: Floppy disk
56 SOFTWARE: PDB
57 CURRENT APPLICATION DATA: 08/09/225,224
58 PUBLICATION NUMBER: 08/09/225,224
59 CLASSIFICATION: 530
60 ATTORNEY/AGENT INFORMATION:
61 REGISTRATION NUMBER: 32,762
62 REFERENCE/DOCKET NUMBER: 15280-193
63 TELEPHONE: (415) 543-6600
64 TELEFAX: (415) 543-5043
65 INFORMATION FOR SEQ ID NO: 31:
66 LENGTH: 39 base pairs
67 TYPE: nucleic acid
68 TOPOLOGY: linear
69
70 MOLECULE TYPE: DNA (primer)
71
72 US-08-722-258-31
73
74 Query Match 17.8% Score 16.6; DB 1; Length 39;
75 Best Local Similarity 17.0%; Pred. No. 7,3e+02;
76 Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
77
78 43 TTCCACCTCCGAGATGATCTGCGCGC 73
79
80 DB 35 TCTCAGCTCCGAGATGATCTGCGCGC 5
81
82 RESULT 5
83 Sequence 31: Application PC/US9504468
84 GENERAL INFORMATION:
85 TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND
86 PROTEIN BINDING DOMAINS
87 NUMBER OF SEQUENCES: 59
88 COMPLETION DATE: 08-APR-1994
89 ADDRESS: Townsend and Townsend Knorrie and Crew
90 STREET: Seagate Street, Tower, One Market Plaza
91 CITY: San Francisco
92 STATE: CA
93 COUNTRY: US
94
95 INT: 94111-3934
96 COMPILED BY: PDB
97 MEDIUM TYPE: Floppy disk
98 SOFTWARE: PDB
99 CURRENT APPLICATION DATA: 08/09/225,224
100 PUBLICATION NUMBER: 08/09/225,224
101 CLASSIFICATION: 530
102 ATTORNEY/AGENT INFORMATION:
103 REGISTRATION NUMBER: 32,762
104 REFERENCE/DOCKET NUMBER: 15280-193
105 TELEPHONE: (415) 543-6600
106 TELEFAX: (415) 543-5043
107 INFORMATION FOR SEQ ID NO: 31:
108 LENGTH: 39 base pairs
109 TYPE: nucleic acid
110 TOPOLOGY: linear
111
112 MOLECULE TYPE: DNA (primer)
113
114 PC-0895-0468-31
115
116 Query Match 17.8% Score 16.6; DB 5; Length 39;
117 Best Local Similarity 17.0%; Pred. No. 7,3e+02;
118 Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```

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1 FILING DATE: 08-APR-1995
2 PDB: 94111-3934
3 APPLICATION NUMBER: US 08/725,224
4 FILING DATE: 08-APR-1994
5 ADDRESS: Townsend and Townsend Knorrie and Crew
6 NAME: Robert, Ellen, Laurel
7 REGISTRATION NUMBER: 32,762
8 REFERENCE/DOCKET NUMBER: 015280-19310005
9 TELEPHONE: (415) 576-0200
10 TELEFAX: (415) 576-0200
11 INFORMATION FOR SEQ ID NO: 31:
12 LENGTH: 39 base pairs
13 STRANDEDNESS: C
14 TOPOLOGY: linear
15
16 MOLECULE TYPE: DNA
17 NAME/SEQ: 1, 39
18 LOCATIONS: 1, 39
19 US-08-722-258-31
20
21 Query Match 17.8% Score 16.6; DB 3; Length 39;
22 Best Local Similarity 17.0%; Pred. No. 7,3e+02;
23 Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
24
25 43 TTCCACCTCCGAGATGATCTGCGCGC 73
26
27 DB 35 TCTCAGCTCCGAGATGATCTGCGCGC 5
28
29 RESULT 5
30 Sequence 31: Application PC/US9504468
31 GENERAL INFORMATION:
32 TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND
33 PROTEIN BINDING DOMAINS
34 NUMBER OF SEQUENCES: 59
35 COMPLETION DATE: 08-APR-1994
36 ADDRESS: Townsend and Townsend Knorrie and Crew
37 STREET: Seagate Street, Tower, One Market Plaza
38 CITY: San Francisco
39 STATE: CA
40 COUNTRY: US
41
42 INT: 94111-3934
43 COMPILED BY: PDB
44 MEDIUM TYPE: Floppy disk
45 SOFTWARE: PDB
46 CURRENT APPLICATION DATA: 08/09/225,224
47 PUBLICATION NUMBER: 08/09/225,224
48 CLASSIFICATION: 530
49 ATTORNEY/AGENT INFORMATION:
50 REGISTRATION NUMBER: 32,762
51 REFERENCE/DOCKET NUMBER: 15280-193
52 TELEPHONE: (415) 543-6600
53 TELEFAX: (415) 543-5043
54 INFORMATION FOR SEQ ID NO: 31:
55 LENGTH: 39 base pairs
56 TYPE: nucleic acid
57 TOPOLOGY: linear
58
59 MOLECULE TYPE: DNA (primer)
60
61 PC-0895-0468-31
62
63 Query Match 17.8% Score 16.6; DB 5; Length 39;
64 Best Local Similarity 17.0%; Pred. No. 7,3e+02;
65 Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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07 43 FTTCMAGCMTGACGTCTGCGCCGCG 73
 35 FTTCMAGCMTGACGTCTGCGCCGCG 5

RESULT 6

US-08-198-670A-34

Sequence 34: Application US/08198670A

GENERAL INFORMATION:

APPLICANT: GOLD, LARRY

REFERENCE: 97/14,131

TITLE OF INVENTION: METHOD FOR SELECTING NUCLEIC ACIDS

ON THE BASIS OF STRUCTURE

CORRESPONDENCE ADDRESS:

ADDRESSEE: Swanson & Braselton, L.L.C.

STREET: Englewood, Prindle Avenue, Suite 200

CITY: Englewood

STATE: Colorado

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette 3.5 inch

SOFTWARE: WordPerfect 6.0 for Windows

OPERATING SYSTEM: MS-DOS

APPLICATION NUMBER: US/08198, 670A

FILING DATE: 22-FEBRUARY-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/960,093

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/14,131

PRIOR APPLICATION DATA: 1991

APPLICATION NUMBER: 07/536,438

ATTORNEY/AGENT INFORMATION:

NAME: Barry J. Swanson

REGISTRATION NUMBER: 31,215

TELEPHONE: (310) 793-3133

TELECOMMUNICATION INFORMATION:

INFORMATION FOR SEQ ID NO: 33,34:

SEQUENCE CHARACTERISTICS:

LENGTH: 49 base pairs

TYPE: nucleic acid

STANDARDNESS: single

TOPOLAGY: linear

TITLE OF INVENTION: Fibroblast Growth Factors
 NUMBER OF SEQUENCES: 227
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Swanson & Braselton, L.L.C.
 STREET: Englewood, Prindle Avenue, Suite 200
 CITY: Englewood
 STATE: Colorado
 COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette 3.5 inch, 1.44 MB storage

SOFTWARE: WordPerfect 5.1

OPERATING SYSTEM: MS-DOS

APPLICATION NUMBER: US/08198, 709A

FILING DATE: 02-FEBRUARY-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/195,005

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/214,131

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/256,428

ATTORNEY/AGENT INFORMATION:

NAME: Barry J. Swanson

REGISTRATION NUMBER: NEXO/D

TELEPHONE: (310) 793-3133

TELECOMMUNICATION INFORMATION:

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 50

TYPE: nucleic acid

STANDARDNESS: single

TOPOLAGY: linear

US-08-384-709A-5

QUERY MATCH

US-08-384-709A-5

US-08-384-709A-5

US-08-384-709A-5

US-08-384-709A-5

US-08-384-709A-5

US-08-384-709A-5

US-08-384-709A-5

US-08-384-709A-5

US-08-384-709A-5

US-08-384-709A-5

07 49 CACTATGAGATGATGCTGCGCCGCG 79
 Matches 22: Conservative 0; Mismatches 9; Indels 0; Gaps 0;

US-08-384-709A-5

Sequence 34: Application US/08198670A

GENERAL INFORMATION:

APPLICANT: GOLD, LARRY

REFERENCE: 97/14,131

TITLE OF INVENTION: METHOD FOR SELECTING NUCLEIC ACIDS

ON THE BASIS OF STRUCTURE

CORRESPONDENCE ADDRESS:

ADDRESSEE: Swanson & Braselton, L.L.C.

STREET: Englewood, Prindle Avenue, Suite 200

CITY: Englewood

STATE: Colorado

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette 3.5 inch, 1.44 MB storage

SOFTWARE: WordPerfect 6.0 for Windows

OPERATING SYSTEM: MS-DOS

APPLICATION NUMBER: US/08198, 670A

FILING DATE: 22-FEBRUARY-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/960,093

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/14,131

PRIOR APPLICATION DATA: 1991

APPLICATION NUMBER: 07/536,438

ATTORNEY/AGENT INFORMATION:

NAME: Barry J. Swanson

REGISTRATION NUMBER: 31,215

TELEPHONE: (310) 793-3133

TELECOMMUNICATION INFORMATION:

INFORMATION FOR SEQ ID NO: 33,34:

SEQUENCE CHARACTERISTICS:

LENGTH: 49 base pairs

TYPE: nucleic acid

STANDARDNESS: single

TITLE OF INVENTION: Fibroblast Growth Factors
 NUMBER OF SEQUENCES: 227
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Swanson & Braselton, L.L.C.
 STREET: Englewood, Prindle Avenue, Suite 200
 CITY: Englewood
 STATE: Colorado
 COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette 3.5 inch, 1.44 MB storage

SOFTWARE: WordPerfect 5.1

OPERATING SYSTEM: MS-DOS

APPLICATION NUMBER: US/08198, 709A

FILING DATE: 02-FEBRUARY-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/195,005

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/214,131

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/256,428

ATTORNEY/AGENT INFORMATION:

NAME: Barry J. Swanson

REGISTRATION NUMBER: NEXO/D

TELEPHONE: (310) 793-3133

TELECOMMUNICATION INFORMATION:

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 50

TYPE: nucleic acid

STANDARDNESS: single

TOPOLAGY: linear

US-08-384-709A-5

QUERY MATCH

US-08-384-709A-5

US-08-384-709A-5

US-08-384-709A-5

US-08-384-709A-5

US-08-384-709A-5

US-08-384-709A-5

US-08-384-709A-5

US-08-384-709A-5

US-08-384-709A-5

US-08-384-709A-5

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COMPILED: 100 COMPILATION
OPERATING SYSTEM: MS-DOS
SOFTWARE: wordperfect 6.0
CURRENT APPLICATION DATA:
PILING DATE: 08-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PILING DATE: 10-FEBRUARY-1994
APPLICATION NUMBER: 08/795.005
PILING DATE: 22-APRIL-1993
PRIOR APPLICATION DATA:
PILING DATE: 28-MARCH-1994
PILING DATE: 07/214.131
PRIOR APPLICATION DATA:
PILING DATE: 11-NOVEMBER-1992
APPLICATION NUMBER: 07/214.131
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/256.428
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Searson
REFERENCE/DOCKET NUMBER: NEXOT/ACT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (310) 313-1333
TELEFAX: (310) 313-1333
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STANDARDNESS: single
US-08-687-421-5 11mer

Query Match
Sequence Similarity 7.6%; Pred. No. 6.64-42;
Matches 22: Conservative 0; Mismatches 9; Indels 0; Gaps 0;

DB 49 CAGTACGAGTACTGCTGCGAGCTGCTGCGAG
US-08-497-001B-19/c 17.8%; Score 16.6; DB 4; Length 50;
Sequence Similarity 7.6%; Pred. No. 6.64-42;
Matches 22: Conservative 0; Mismatches 9; Indels 0; Gaps 0;

DB 20 CAGTACGAGTACTGCTGCGAGCTGCTGCGAG
RESULT 9
US-08-497-001B-19/c
Patent No. 6228621
GENERAL INFORMATION:
COMPILED: 100 COMPILATION US/08/957.001B
APPLICANT: Madaio, Michael V.
APPLICANT: Madaio, David B.
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESSES:
ADDRESSER: Woodcock Washburn Kutz Mocklewicz & No. 6228621115
CITY: Philadelphia
STATE: Pennsylvania
ZIP: 19103
COMPILED: 100 COMPILATION
COMPILED: 100 COMPILATION
OPERATING SYSTEM: Windows
SOFTWARE: wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/957.001B

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PILING DATE: 23-OCT-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039.592
PILING DATE: 08-MAY-1996
CLASSIFICATION: 424 1996
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 33.229
REFERENCE/DOCKET NUMBER: UPN-3303
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3490
TELEFAX: 215-568-3499
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 47 base pairs
TYPE: nucleic acid
STANDARDNESS: single
TOPOLLOGY: linear
US-08-497-001B-19 17.6%; Score 16.4; DB 4; Length 47;
Sequence Similarity 6.3%; Pred. No. 6.64-42;
Matches 21: Conservative 2; Mismatches 13; Indels 0; Gaps 0;

DB 55 CAGATGTCAGTCTGCTGCGAGAACTGAGCT 92
US-08-496-301-19/c
Sequence 19: Application US/0946301
GENERAL INFORMATION:
COMPILED: 100 COMPILATION US/0946301
APPLICANT: Williams, William V.
APPLICANT: Madaio, David B.
TITLE OF INVENTION: IMPROVED VACCINES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESSES:
ADDRESSER: Woodcock Washburn Kutz Mocklewicz & No. 62485515
CITY: Philadelphia
STATE: Pennsylvania
ZIP: 19103
COMPILED: 100 COMPILATION
COMPILED: 100 COMPILATION
OPERATING SYSTEM: Windows
SOFTWARE: wordperfect
CURRENT APPLICATION DATA:
PILING DATE: 09/09/96.301
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PILING DATE: 23-OCT-1997
APPLICATION NUMBER: US 60/029.592
CLASSIFICATION: 1997-1996
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 33.229
REFERENCE/DOCKET NUMBER: UPN-3303
TELEPHONE: 215-568-3490
TELEFAX: 215-568-3499
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 47 base pairs
TYPE: nucleic acid
STANDARDNESS: single
TOPOLLOGY: linear
US-08-496-301-19/c 17.6%; Score 16.4; DB 4; Length 47;
Sequence Similarity 6.3%; Pred. No. 6.64-42;
Matches 21: Conservative 2; Mismatches 13; Indels 0; Gaps 0;

DB 46 CAGATGTCAGTCTGCTGCGAGAACTGAGCT 92

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? TITLE OF INFORMATION: Braxton Polymorphisms
? NAME OF INFORMATION: 17
? CORRESPONDENCE ADDRESS: 173
? ADDRESSER: Townsend and Townsend and Crew LLP
? CITY: San Francisco
? STATE: California
? ZIP: 94111-3814
? ATTORNEY/AGENT INFORMATION: 33
? NAME: Liebenchuev, Joe
? TELEPHONE: 415 576-0200
? REFERENCE/DOCKET NUMBER: 08547-03010005
? OTHER INFORMATION: /notice "detection polymorphism"
? DESCRIPTION: SEQ ID NO: 43:
? SOFTWARE: PASTED FOR Windows Version 2.0
? APPLICATION NUMBER: US/09/813 507
? FILING DATE: 07-Nov-1997
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/66/032,069
? FILING DATE: 01-Dec-1996
? NAME: Liebenchuev, Joe
? TELEPHONE: 415 576-0200
? REGISTRATION NUMBER: 37,505
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415 576-0200
? FAX: 415 576-0200
? INFORMATION FOR SEQ ID NO: 43:
? SEQUENCE CHARACTERISTICS:
? TYPE: nucleic acid
? STRANDNESS: single
? FEATURE:
? NAME/KEY: variation
? LOCATION: replace(21, **)
? OTHER INFORMATION: /notice "detection polymorphism"
? ORIGIN: 32 TTGCACCTGTGGACATGTACATGTC 6
?
? Query Match
? Beat Local Similarity 17.0%, Score 15.8, IR 3, Length 42:
? Matches 20: Conservative 0, Mismatches 7, Indels 0, Gaps 0:
?
? 43 TTGCACCTGTGGACATGTACATGTC 6
? 32 TTGCACCTGTGGACATGTACATGTC 6

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? RESULT 15
? US-09-843-453-45/C
? Sequence 45, Application US/09/464433
? Patent No. 635866
? GENERAL INFORMATION:
? APPLICANT: Landry, Ronald S.
? ADDRESSER: Landry, Ronald S.
? TITLE OF INFORMATION: Braxton Polymorphisms
? NUMBER OF SEQUENCES: 173
? CORRESPONDENCE ADDRESS: 173
? STREET: Two Buharadero Center, Eighth Floor
? CITY: San Francisco
? STATE: California
? ZIP: 94111-3814
? ATTORNEY/AGENT INFORMATION: 33
? NAME: Liebenchuev, Joe
? TELEPHONE: 415 576-0200
? REFERENCE/DOCKET NUMBER: 08547-03010005
? OTHER INFORMATION: /notice "detection polymorphism"
? DESCRIPTION: SEQ ID NO: 43:
? SOFTWARE: PASTED FOR Windows Version 2.0
? APPLICATION NUMBER: US/09/813 507
? FILING DATE: 07-Nov-1997
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/66/032,069
? FILING DATE: 01-Dec-1996
? NAME: Liebenchuev, Joe
? TELEPHONE: 415 576-0200
? REGISTRATION NUMBER: 37,505
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415 576-0200
? FAX: 415 576-0200
? INFORMATION FOR SEQ ID NO: 43:
? SEQUENCE CHARACTERISTICS:
? TYPE: nucleic acid
? STRANDNESS: single
? FEATURE:
? NAME/KEY: variation
? LOCATION: replace(21, **)
? OTHER INFORMATION: /notice "detection polymorphism"
? ORIGIN: 32 TTGCACCTGTGGACATGTACATGTC 6
?
? Query Match
? Beat Local Similarity 17.0%, Score 15.8, IR 4, Length 42:
? Matches 20: Conservative 0, Mismatches 7, Indels 0, Gaps 0:
?
? 43 TTGCACCTGTGGACATGTACATGTC 6
? 32 TTGCACCTGTGGACATGTACATGTC 6

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? RESULT 16
? US-08-368-395-8/C
? Sequence 45, Application US/08/368395
? Patent No. 5631150
? GENERAL INFORMATION:
? APPLICANT: Wasyliuk, Andrey N.
? ADDRESSER: Wasyliuk, Andrey N.
? TITLE OF INFORMATION: Braxton Polymorphisms
? NUMBER OF SEQUENCES: 8
? CORRESPONDENCE ADDRESS: 1100 New York Avenue
? STREET: 1100 New York Avenue
? CITY: Washington
? STATE: D.C.
? ZIP: 20005-3934
? ATTORNEY/AGENT INFORMATION: 33
? NAME: Liebenchuev, Joe
? TELEPHONE: 415 576-0200
? REFERENCE/DOCKET NUMBER: 08547-03010005
? OTHER INFORMATION: /notice "detection polymorphism"
? DESCRIPTION: SEQ ID NO: 43:
? SOFTWARE: PASTED FOR Windows Version 2.0
? APPLICATION NUMBER: US/08/368 395
? FILING DATE: 01-Nov-1997
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/08/110 672
? FILING DATE: 01-Nov-1997
? NAME: Liebenchuev, Joe
? TELEPHONE: 415 576-0200
? REGISTRATION NUMBER: 33,851
? TELECOMMUNICATION INFORMATION:

```


INFORMATION FOR SEQ ID NO: 285;
 SEQUENCE CHARACTERISTICS:
 LENGTH: 41 base pairs
 TYPE: double
 STRANDS: single
 TOPOLOGY: linear
 FEATURE TYPE: RNA
 OTHER INFORMATION: All pyrimidines are 2'-fluoro (2'-f) modified
 PCT-0836-08014-205

Query Match 16.6% Score 15.4; DB 5; Length 41;
 Best Local Similarity 32.0%; Pred. No. 2.3e+03;

Matches 13; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

30 GAAATCTCTGGTTCATCAATG 54
 4 GACACGCGGCGGCGACGACGACG 28

RESULT 22
 US-08-454-557C-63/c

Sequence 63; Application US/0845457C

GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

INVENTOR: de la Monte, Jack R.

TITLE OF INVENTION: Throad Protein Gene Expression and Detection

NUMBER OF SEQUENCES: 121

ADDRESSER: Sterne, Kessler, Goldstein & Fox P.L.L.C.

STREET: 1100 New York Avenue, Suite 600

STATE: D.C.

COUNTRY: U.S.A.

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

FILING DATE: 30-MAY-1995

CLASSIFICATION: 314

ATTORNEY/AGENT INFORMATION:

NAME: J. K. KESSLER

REGISTRATION NUMBER: 36,203

REFERENCE/DOC# NUMBER: 0609,3840003

TELEPHONE: (202) 371-2500

INVENTOR: de la Monte, Suzanne

TITLE OF INVENTION: Throad Protein Gene Expression and Detection

NUMBER OF SEQUENCES: 121

ADDRESSER: Sterne, Kessler, Goldstein & Fox P.L.L.C.

STREET: 1100 New York Avenue, Suite 600

STATE: Washington

COUNTRY: U.S.A.

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

FILING DATE: 30-MAY-1995

CLASSIFICATION: 314

ATTORNEY/AGENT INFORMATION:

NAME: J. K. KESSLER

REGISTRATION NUMBER: 36,203

REFERENCE/DOC# NUMBER: 0609,3840003

TELEPHONE: (202) 371-2500

INVENTOR: de la Monte, Suzanne

TITLE OF INVENTION: Throad Protein Gene Expression and Detection

NUMBER OF SEQUENCES: 121

ADDRESSER: Sterne, Kessler, Goldstein & Fox P.L.L.C.

STREET: 1100 New York Avenue, Suite 600

STATE: Washington

COUNTRY: U.S.A.

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

FILING DATE: 30-MAY-1995

CLASSIFICATION: 530

Patent No. 5946514

GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

INVENTOR: de la Monte, Jack R.

TITLE OF INVENTION: Throad Protein Gene Expression and Detection

NUMBER OF SEQUENCES: 121

ADDRESSER: Sterne, Kessler, Goldstein & Fox P.L.L.C.

STREET: 1100 New York Avenue, Suite 600

STATE: Washington

COUNTRY: U.S.A.

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

FILING DATE: 30-MAY-1994

CLASSIFICATION: 433

ATTORNEY/AGENT INFORMATION:

NAME: J. K. KESSLER

REGISTRATION NUMBER: 36,203

REFERENCE/DOC# NUMBER: 0609,3840002

TELEPHONE: (202) 371-2500

INVENTOR: de la Monte, Suzanne

TITLE OF INVENTION: Throad Protein Gene Expression and Detection

NUMBER OF SEQUENCES: 121

ADDRESSER: Sterne, Kessler, Goldstein & Fox P.L.L.C.

STREET: 1100 New York Avenue, Suite 600

STATE: Washington

COUNTRY: U.S.A.

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

FILING DATE: 30-MAY-1994

CLASSIFICATION: 433

ATTORNEY/AGENT INFORMATION:

NAME: J. K. KESSLER

REGISTRATION NUMBER: 36,203

REFERENCE/DOC# NUMBER: 0609,3840002

TELEPHONE: (202) 371-2500

INVENTOR: de la Monte, Suzanne

TITLE OF INVENTION: Throad Protein Gene Expression and Detection

NUMBER OF SEQUENCES: 121

ADDRESSER: Sterne, Kessler, Goldstein & Fox P.L.L.C.

STREET: 1100 New York Avenue, Suite 600

STATE: Washington

COUNTRY: U.S.A.

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

FILING DATE: 30-MAY-1994

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: J. K. KESSLER

REGISTRATION NUMBER: 36,203

REFERENCE/DOC# NUMBER: 0609,3840002

TELEPHONE: (202) 371-2500

INVENTOR: de la Monte, Suzanne

TITLE OF INVENTION: Throad Protein Gene Expression and Detection

NUMBER OF SEQUENCES: 121

ADDRESSER: Sterne, Kessler, Goldstein & Fox P.L.L.C.

STREET: 1100 New York Avenue, Suite 600

STATE: Washington

COUNTRY: U.S.A.

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

FILING DATE: 30-MAY-1994

CLASSIFICATION: 530

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 FILING DATE: Herewith
 CLASSIFICATION: 424
 NAME/ALIAS INFORMATION:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212/377-9550
 TELEFAX: 42523
 TELETYPE: 42523
 INFORMATION FOR SEQ ID NO: 133:
 SEQ LENGTH: 41 base pairs
 TYPE: nucleic acid
 TOPOLOGY: double
 MOLECULE TYPE: DNA (genomic)
 HYDROLYTICAL: NO
 ORGANISM: Bovine respiratory syncytial virus
 ORIGINAL SOURCE:
 STRAIN: 715

Query Match Similarity 15 14; Score 15; DB 3; Length 41;
 Matches 21; Conservative 0; Mismatches 10; Indels 0;

DB 40 PATCTCTGATTATTAAGATGCGTATGAG 10

RESULT 36
 US-08-486-946C-70/C
 Patent No. 6221961
 GENERAL INFORMATION: US/08/6596C
 APPLICANT: COCHLIN, Mark D.
 TITLE OF INVENTION: Recombinant Swinepox Virus
 FILING REFERENCE: 39139-1/4/M; US/09/686-968C
 CURRENT FILING DATE: 1996-07-25
 NUMBER OF SEQ ID NOS: 231
 SEQ ID NO 70
 LENGTH: 41
 ORGANISM: Artificial Sequence
 FEATURE: Artificial Sequence
 OTHER INFORMATION: Description of Artificial Sequence: primer

Query Match Similarity 16 14; Score 15; DB 4; Length 41;
 Matches 21; Conservative 0; Mismatches 10; Indels 0;

DB 33 AATCCGCTGTTTACATCTGCGATATG 63

RESULT 37
 US-08-488-237A-143/C
 Patent No. 6231601
 GENERAL INFORMATION: US/08/69237A

APPLICANT: COCHLIN, Mark D.
 APPLICANT: JUNKER, David E.
 TITLE OF INVENTION: Recombinant Swinepox Virus
 FILING REFERENCE: 39139-1/4/M; US/09/686-968C
 CURRENT FILING DATE: 1996-07-25
 NUMBER OF SEQ ID NOS: 231
 SEQ ID NO 70
 LENGTH: 41
 ORGANISM: Artificial Sequence
 FEATURE: Artificial Sequence
 OTHER INFORMATION: Description of Artificial Sequence: primer

Query Match Similarity 16 14; Score 15; DB 4; Length 41;
 Matches 21; Conservative 0; Mismatches 10; Indels 0;

DB 40 PATCTCTGATTATTAAGATGCGTATGAG 10

RESULT 38
 US-08-672-213-30
 Patent No. 6306449
 GENERAL INFORMATION: US/08/67213
 APPLICANT: NITZMAN, Shlomo
 TITLE OF INVENTION: USE OF HERPETOUS TRANSCRIPTION
 FACTORS IN GENE THERAPY
 ADDRESS: AVID Gene Therapeutics, Inc.
 CITY: Cambridge
 STATE: Massachusetts
 ZIP: 02139-4234

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent Release #1.0, Version #1.30
 APPLICATION NUMBER: US/08/672-213

PILING DATE: 27-JUN-1996
 CLASSIFICATION: 314
 PRIOR APPLICATION DATA:
 PILING DATE: 08-SEP-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/013,614
 ATORNEY/AGENT INFORMATION:
 NAME: BERSTEIN, David L.
 REFERENCE/DOCKET NUMBER: A15
 TELEPHONE: 617-944-0000
 INFORMATION FOR SEQ ID NO: 30:
 SEQUENCE CHARACTERISTICS:
 TYPE: nucleic acid
 STANDARDS: single
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 US-08-672-213-30
 Query Match
 Best Local Similarity 16.1%, Score 15, DB 4, Length 41:
 Matches 21: Conservative 0, Mismatches 10, Indels 0, Gaps 0:
 45 TCACACATCGCAGTCGACATCGCAGCT 75
 ||||| 1 ||||| 11111
 DB 3 TCACACATCGCAGTCGACATCGCAGCT 35

PILING DATE: 27-JUN-1996
 CLASSIFICATION: 314
 PRIOR APPLICATION DATA:
 PILING DATE: 08-SEP-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/013,614
 ATORNEY/AGENT INFORMATION:
 NAME: BERSTEIN, David L.
 REFERENCE/DOCKET NUMBER: A15
 TELEPHONE: 617-944-0000
 INFORMATION FOR SEQ ID NO: 30:
 SEQUENCE CHARACTERISTICS:
 TYPE: nucleic acid
 STANDARDS: single
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 US-08-672-213-30
 Query Match
 Best Local Similarity 16.1%, Score 15, DB 4, Length 41:
 Matches 21: Conservative 0, Mismatches 10, Indels 0, Gaps 0:
 45 TCACACATCGCAGTCGACATCGCAGCT 75
 ||||| 1 ||||| 11111
 DB 3 TCACACATCGCAGTCGACATCGCAGCT 35

PILING DATE: 27-JUN-1996
 CLASSIFICATION: 314
 PRIOR APPLICATION DATA:
 PILING DATE: 08-SEP-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/013,614
 ATORNEY/AGENT INFORMATION:
 NAME: BERSTEIN, David L.
 REFERENCE/DOCKET NUMBER: A15
 TELEPHONE: 617-944-0000
 INFORMATION FOR SEQ ID NO: 30:
 SEQUENCE CHARACTERISTICS:
 TYPE: nucleic acid
 STANDARDS: single
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 US-08-672-213-30
 Query Match
 Best Local Similarity 16.1%, Score 15, DB 4, Length 41:
 Matches 21: Conservative 0, Mismatches 10, Indels 0, Gaps 0:
 45 TCACACATCGCAGTCGACATCGCAGCT 75
 ||||| 1 ||||| 11111
 DB 3 TCACACATCGCAGTCGACATCGCAGCT 35

PILING DATE: 27-JUN-1996
 CLASSIFICATION: 314
 PRIOR APPLICATION DATA:
 PILING DATE: 08-SEP-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/013,614
 ATORNEY/AGENT INFORMATION:
 NAME: BERSTEIN, David L.
 REFERENCE/DOCKET NUMBER: A15
 TELEPHONE: 617-944-0000
 INFORMATION FOR SEQ ID NO: 30:
 SEQUENCE CHARACTERISTICS:
 TYPE: nucleic acid
 STANDARDS: single
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 US-08-672-213-30
 Query Match
 Best Local Similarity 16.1%, Score 15, DB 4, Length 41:
 Matches 21: Conservative 0, Mismatches 10, Indels 0, Gaps 0:
 45 TCACACATCGCAGTCGACATCGCAGCT 75
 ||||| 1 ||||| 11111
 DB 3 TCACACATCGCAGTCGACATCGCAGCT 35

Db 1 000000627C00000000000000000000 31

RESULT 41
US-09-067-615-38
US-09-067-615-38
Patent No. 6309645
GENERAL INFORMATION:
APPLICANT: Jiao, Jiao R.
APPLICANT: Burkhardt, Martin
TITLE OF INVENTION: NEW COMPLEXES AND USES THEREOF
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
STREET: 117 Deerfield Road
CITY: Deerfield
STATE: Illinois
COUNTRY: USA
ZIP: 60015
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/067-615
CLASSIFICATION:
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION NUMBER: 08/596,387
PRIORITY APPLICATION DATE: 08/08/1995
APPLICATION NUMBER: US 08/382,454
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION NUMBER: 1995
APPLICATION NUMBER: US 08/283,302
ATTORNEY/AGENT INFO: 100-1394
NAME: Pearson, Louise S.
REGISTRATION NUMBER: 32,359
REGISTRATION DATE: 08/08/1995
TELEPHONE: (708) 267-5300
TELECOMMUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO: 5376
SEQUENCE CHARACTERISTICS: 38;
LENGTH: 42 base pairs
STRANDS: 2
STRANDBESS: unknown
TOPOLGY: unknown
DB-09-067-615-38
Query Match Similarity: 16.1%; Score 15; DB 4; Length 42;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Db 1 000000627C00000000000000000000 31

APPLICANT: Chavallier, Pierre-Andre
APPLICANT: Jiao, Jiao R.
TITLE OF INVENTION: MIC COMPLEXES AND USES THEREOF
NUMBER OF SEQUENCES: 123
CORRESPONDENCE ADDRESS:
ADDRESSER: Dade International, Inc.
STREET: 1717 Deerfield Road
CITY: Deerfield
STATE: Illinois
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIA TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/067-615
FILING DATE: 31-JUL-1995
CLASSIFICATION:
PRIORITY APPLICATION DATA: US 08/382,454
APPLICATION NUMBER: 1995
FILING DATE: 01-FEB-1995
PRIORITY APPLICATION DATA: US 08/283,302
FILING DATE: 28-JUL-1994
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 32,359
REGISTRATION DATE: 08/08/1995
TELEPHONE: (708) 267-5376
TELECOMMUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO: 38;
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
STRANDS: 2
STRANDBESS: unknown
TOPOLGY: unknown
DB-09-067-615-38
Query Match
DB-09-067-615-38
Sequence 13; Application US/0861935
Patent No. 5710248
APPLICANT: GROCE, CHARLES F.
TITLE OF INVENTION: PEPTIDE TAG FOR IMMUNODTECTION AND
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSER: MERRIN, MANUEL GEBMART & SCHWARTZ, P.A.
STREET: 1717 DEERFIELD ROAD
CITY: MINNEAPOLIS
STATE: MINNESOTA
ZIP: 55401
COMPUTER READABLE FORM:
MEDIA TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/681,935

FILING DATE: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: MCGRAW, WEA H. 492
 REFERENCE/DOCKET NUMBER: 140.00040101
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 612-305-1245
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 TYPE: nucleic acid
 STANDARDS: single
 MOLECULE TYPE: DNA (genomic)
 US-08-681-935-13
 Query Match: 16.1% Score 15; DB 1; Length 45;
 Best Local Similarity: 61.3%; Pred. No. 3.6e+03;
 Matches 24; Conservative 0; Mismatches 15; Indels 0
 30 GACACGCTGCTGGTTCACATCGCATGTCAGTCTG 68
 7 GTCCACGATGCTGCTTCACATCGCATGTCAGTCTG 45
 DB
 RESULT 44
 US-08-939-323-13
 Sequence 13; Application US/0839323
 PATENT NO. 6255462
 APPLICANT: GROSS, CHARLES F.
 TITLE OF INVENTION: METHOD FOR IMMUNODETECTION AND
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ATTORNEY/AGENT INFORMATION:
 NAME: MCGRAW, WEA H. 492
 STREET: 119 NORTH FOURTH STREET, SUITE 203
 CITY: MINNEAPOLIS
 STATE: MINN
 COUNTRY: USA
 ZIP: 55401
 COMPUTER READABLE FORM: 414
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA: Release 41.0; Version 41.30
 APPLICATION NUMBER: US/08/939.323
 FILING DATE: 29-SEP-1997
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/681.935
 ATTORNEY/AGENT INFORMATION:
 NAME: MCGRAW, WEA H. 492
 REFERENCE/DOCKET NUMBER: 140.00040102
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (612) 305-1245
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 TYPE: nucleic acid
 STANDARDS: single
 MOLECULE TYPE: OTHER nucleic acid
 US-08-939-323-13
 Query Match: 16.1% Score 15; DB 4; Length 45;
 Best Local Similarity: 61.3%; Pred. No. 3.6e+03;

Matches 24; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
 30 GACACGCTGCTGGTTCACATCGCATGTCAGTCTG 68
 7 GTCCACGATGCTGCTTCACATCGCATGTCAGTCTG 45
 DB
 RESULT 45
 US-08-584-040-569/C
 Sequence 3659; Application US/0858400
 GENERAL INFORMATION:
 APPLICANT: Payco, Pamela
 APPLICANT: McGraw, James T.
 TITLE OF INVENTION: METHOD AND REAGENT FOR THE
 TITLE OF INVENTION: CONDITIONS RELATED TO LEBELS
 TITLE OF INVENTION: OF VASCULAR BIOTHELIAL
 NUMBER OF SEQUENCES: 8502
 CORRESPONDENCE ADDRESS:
 ADDRESS: 1001 N. LEX
 STREET: Suite 4700
 CITY: Los Angeles
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM: 414
 OPERATING SYSTEM: PC-DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA: US/08/584.040
 FILING DATE: January 11, 1996
 CLASSIFICATION: 514
 APPLICATION NUMBER: 60/005.974
 FILING DATE: October 26, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: MCGRAW, WEA H. 492
 REFERENCE/DOCKET NUMBER: 32.327
 TELEPHONE: (213) 489-1600
 INFORMATION FOR SEQ ID NO: 3659:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 27 base pairs
 STANDARDS: single
 MOLECULE TYPE: linear
 OTHER INFORMATION: The letter 'N' represents the stem II region
 US-08-584-040-569/C
 Query Match: 15.9% Score 14.8; DB 4; Length 27;
 Best Local Similarity: 70.4%; Pred. No. 3.4e+03;
 Matches 15; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 61 GTGACGTCGCGCTCCCAAAATAT 87
 27 GTGACGTCGTCACAAATAT 1

Sequence 5069 Application US/08984040
 Patent No. 616639
 GENERAL INFORMATION:
 APPLICANT: Pacy, Pamela
 ADDRESS: 1000 16th Street, N.E., Suite 500
 APPLICANT: Stinchcomb, Dan T.
 ADDRESS: 1000 16th Street, N.E., Suite 500
 CITY: Washington
 STATE: D.C.
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patscan Release #1.0, Version #1.30
 CORRESPONDENCE ADDRESS:
 APPLICANT: Pacy, Pamela
 ADDRESS: 1000 16th Street, N.E., Suite 500
 CITY: Washington
 STATE: D.C.
 ZIP: 20007-5109
 STREET: Suite 4700
 CITY: San Francisco
 STATE: California
 COUNTRY: U.S.A.
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 APPLICATION NUMBER: US/08/984 040
 FILING DATE: January 11, 1996
 CLASSIFICATION DATA:
 PRIORITY NUMBER: 61
 APPLICATION NUMBER: 60/005 974
 FILING DATE: October 26, 1995
 NAME: Mathburg, Richard J.
 REGISTRATION NUMBER: 32,327
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: 67(213) 955-0440
 SEQUENCE CHARACTERISTICS:
 INFORMATION FOR SEQ ID NO: 5068:
 TYPE: nucleic acid
 STANDARDS: single
 FEATURES: linear
 OTHER INFORMATION: The letter "N" represents the stem II region
 of the protein.
 US-08-584 040-5068
 Query Match 15.34% Score 14.8; DB 4; Length 27;
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Caps 0;
 Db 61 CTGACCTGTCGCCACCAACAAACCTT 87
 US-08-332 562A-33
 Patent No. 5285593
 GENERAL INFORMATION:
 APPLICANT: KICKWELZ, Ian F. C.
 ADDRESS: 1000 16th Street, N.E., Suite 500
 APPLICANT: HIRS, Margaret L.
 ADDRESS: 1000 16th Street, N.E., Suite 500
 CITY: Washington
 STATE: D.C.
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patscan Release #1.0, Version #1.30
 CORRESPONDENCE ADDRESS:
 APPLICANT: KICKWELZ, Ian F. C.
 ADDRESS: 1000 16th Street, N.E., Suite 500
 CITY: Washington
 STATE: D.C.
 ZIP: 20007-5109
 STREET: Suite 4700
 CITY: San Francisco
 STATE: California
 COUNTRY: U.S.A.
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 APPLICATION NUMBER: US/08/984 040
 FILING DATE: January 11, 1996
 CLASSIFICATION DATA:
 PRIORITY NUMBER: 61
 APPLICATION NUMBER: 60/005 974
 FILING DATE: October 26, 1995
 NAME: Mathburg, Richard J.
 REGISTRATION NUMBER: 32,327
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: 67(213) 955-0440
 SEQUENCE CHARACTERISTICS:
 INFORMATION FOR SEQ ID NO: 5068:
 TYPE: nucleic acid
 STANDARDS: single
 FEATURES: linear
 OTHER INFORMATION: The letter "N" represents the stem II region
 of the protein.
 US-08-584 040-5068

TITLE OF INVENTION: RECEPTOR FOR IMMUNOGLOBULIN
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 APPLICANT: Coley, S. Lardner
 ADDRESS: 1000 16th Street, N.E., Suite 500
 CITY: Washington
 STATE: D.C.
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patscan Release #1.0, Version #1.30
 CORRESPONDENCE ADDRESS:
 APPLICANT: Coley, S. Lardner
 ADDRESS: 1000 16th Street, N.E., Suite 500
 CITY: Washington
 STATE: D.C.
 ZIP: 20007-5109
 STREET: Suite 4700
 CITY: San Francisco
 STATE: California
 COUNTRY: U.S.A.
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patscan Release #1.0, Version #1.30
 CORRESPONDENCE ADDRESS:
 APPLICANT: Coley, S. Lardner
 ADDRESS: 1000 16th Street, N.E., Suite 500
 CITY: Washington
 STATE: D.C.
 ZIP: 20007-5109
 STREET: Suite 4700
 CITY: San Francisco
 STATE: California
 COUNTRY: U.S.A.
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 APPLICATION NUMBER: US/08/984 040
 FILING DATE: January 11, 1996
 CLASSIFICATION DATA:
 PRIORITY NUMBER: 61
 APPLICATION NUMBER: 60/005 974
 FILING DATE: October 26, 1995
 NAME: Mathburg, Richard J.
 REGISTRATION NUMBER: 32,327
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: 67(213) 955-0440
 SEQUENCE CHARACTERISTICS:
 INFORMATION FOR SEQ ID NO: 33:
 TYPE: nucleic acid
 STANDARDS: single
 FEATURES: linear
 OTHER INFORMATION: The letter "N" represents the stem II region
 of the protein.
 US-08-332 562A-33
 Query Match 15.34% Score 14.8; DB 2; Length 30;
 Matches 19; Conservative 0; Mismatches 7; Indels 0; Caps 0;
 Db 44 TTGACATATGCGATGCGATGCTGTC 69
 US-08-813 507-147
 Patent No. 614116
 GENERAL INFORMATION:
 APPLICANT: Barford
 ADDRESS: 1000 16th Street, N.E., Suite 500
 APPLICANT: Spasally, Ronald S.
 ADDRESS: 1000 16th Street, N.E., Suite 500
 CITY: Washington
 STATE: D.C.
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patscan Release #1.0, Version #1.30
 CORRESPONDENCE ADDRESS:
 APPLICANT: Barford
 ADDRESS: 1000 16th Street, N.E., Suite 500
 CITY: Washington
 STATE: D.C.
 ZIP: 20007-5109
 STREET: Suite 4700
 CITY: San Francisco
 STATE: California
 COUNTRY: U.S.A.
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patscan Release #1.0, Version #1.30
 CORRESPONDENCE ADDRESS:
 APPLICANT: Barford
 ADDRESS: 1000 16th Street, N.E., Suite 500
 CITY: Washington
 STATE: D.C.
 ZIP: 20007-5109
 STREET: Suite 4700
 CITY: San Francisco
 STATE: California
 COUNTRY: U.S.A.
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 APPLICATION NUMBER: US/08/984 040
 FILING DATE: January 11, 1996
 CLASSIFICATION DATA:
 PRIORITY NUMBER: 61
 APPLICATION NUMBER: 60/005 974
 FILING DATE: October 26, 1995
 NAME: Mathburg, Richard J.
 REGISTRATION NUMBER: 32,327
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: 67(213) 955-0440
 SEQUENCE CHARACTERISTICS:
 INFORMATION FOR SEQ ID NO: 33:
 TYPE: nucleic acid
 STANDARDS: single
 FEATURES: linear
 OTHER INFORMATION: The letter "N" represents the stem II region
 of the protein.
 US-08-332 562A-33

PATENT NO. 6265561
 GENERAL INFORMATION:
 APPLICANT: Melisilbloom, M.D., Richard M.
 APPLICANT: Wood, Thomas C.
 APPLICANT: Ottewill, Diana B.
 FILE REFERENCE: 07/09/11801 US/09/167,681A
 CURRENT FILING DATE: 1998-10-07
 INVENTOR: Melisilbloom, M.D., Richard M.
 SOFTWARE: Resisted for Windows Version 3.0
 SEQ ID NO: 6
 TYPE: DNA
 ORGANISM: Artificial Sequence
 OTHER INFORMATION: primer
 US-09-167,681-6

Query Match 15 7% Score 14.6; DB 4; Length 25;
 Best Local Similarity: 81.0%; Pct: No. 1; Seq: 3;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OR
 15 CACTGCTCCGCGCCCAAT 35
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 DB 1 CCACTGCTCCGCGCCCAAT 21

RESULT 52
 US-09-167,681-12
 Sequence 12; Application US/09167681A
 PATENT NO. 6265561
 GENERAL INFORMATION:
 APPLICANT: Melisilbloom, M.D., Richard M.
 APPLICANT: Wood, Thomas C.
 APPLICANT: Ottewill, Diana B.
 FILE REFERENCE: 07/09/11801 US/09/167,681A
 CURRENT FILING DATE: 1998-10-07
 INVENTOR: Melisilbloom, M.D., Richard M.
 SOFTWARE: Resisted for Windows Version 3.0
 SEQ ID NO: 12
 TYPE: DNA
 ORGANISM: Artificial Sequence
 OTHER INFORMATION: primer
 US-09-167,681-12

Query Match 15 7% Score 14.6; DB 4; Length 25;
 Best Local Similarity: 81.0%; Pct: No. 3; Seq: 3;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OR
 15 CACTGCTCCGCGCCCAAT 35
 ||| ||||| ||||| |||||
 DB 1 CCACTGCTCCGCGCCCAAT 21

CORRESPONDENCE ADDRESS:
 APPLICANT: Melisilbloom, M.D., Richard M.
 STREET: 3000 K Street, N.W., Suite 500
 CITY: Washington
 STATE: DC
 ZIP: 20007-5109
 COUNTRY: USA
 COMMUNICATIONS:
 TELEPHONE: 202-775-1995
 FAX: 202-775-1996
 OPERATING SYSTEM: PC-DOS/MS-DOS
 COMPUTER: IBM PC compatible
 CURRENT APPLICATION DATA: Release 31.0, Version 41.30
 APPLICATION NUMBER: US/09/557,128
 CLASSIFICATION: 25 1596
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO 97/49510/005
 PRIOR APPLICATION DATA: 1995
 APPLICATION NUMBER: JP 7-123287
 PRIOR APPLICATION DATA: 1995
 APPLICATION NUMBER: JP 6-288823
 PRIOR APPLICATION DATA: 1994
 APPLICATION NUMBER: JP 6-135015
 FILING DATE: 25-MAY-1994
 APPLICATION NUMBER: 1994-05-1994
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 29,768
 TELEPHONE: (202) 672-5100
 TELECOMMUNICATION INFORMATION:
 TELEFAX: 041351672-5199
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 30
 TYPE: nucleic acid
 STRANDNESS: single
 US-09-557,128-23

Query Match 15 7% Score 14.6; DB 2; Length 31;
 Best Local Similarity: 81.0%; Pct: No. 4; Seq: 3;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OR
 4 CCGGACGACGCTATTCG 24
 ||| ||||| ||||| |||||
 DB 10 CCGGACGACGCTATTCG 30

RESULT 54
 US-09-557,128-23
 Sequence 15; Application US/09557128
 PATENT NO. 6018103
 GENERAL INFORMATION:
 APPLICANT: Melisilbloom, M.D., Richard M.
 APPLICANT: Ottewill, Diana B.
 TITLE OF INVENTION: Chimeric Plant Genes possessing
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS: 1092 K Street, N.W.
 STREET: 1092 K Street, N.W.
 CITY: Research Triangle Park
 STATE: NC
 ZIP: 27709
 COUNTRY: USA
 COMMUNICATIONS:
 TELEPHONE: 919-677-0144
 COMPUTER: IBM PC compatible


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? INFORMATION FOR SEQ ID NO: 9:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 35 base pairs
? TYPE: DNA
? STRANDEDNESS: single
? TOPOLOGY: linear
? Molecule type: DNA (genomic)
? US-08-683-877-9

Query Match
? Best Local Similarity 15.7% Score 14.6; DB 1; Length 35;
? Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

? 7 GAGCGACCCGCTCCGCGGTCAAGT 35
? 1 | | | | | | | | | | | | | | | | | |
? Db 33 GACGACCCGCGGTCCCGGTCAAGT 5

RESULT 38
? US-09-242-9504-10
? Sequence 38: Application US/09342590A
? Patent No. 634531
? GENERAL INFORMATION:
? INVENTOR: KATZ
? APPLICANT: KATZ
? TITLE OF INVENTION: YEAST VECTOR AND METHOD OF PRODUCING PROTEINS USING THE
? FILE REFERENCE NO.: SAME
? CURRENT APPLICATION NUMBER: US/09/242,690A
? CURRENT FILING DATE: 1999-02-23
? PRIOR FILING DATE: 1997-08-22
? PRIOR APPLICATION NUMBER: JP 97/10652
? NUMBER OF SEQ ID NOS: 66
? SOFTWARE: Patella Ver. 2.1
? LENGTH: 38
? TYPE: DNA
? Molecule type: Artificial Sequence
? OTHER INFORMATION: Description of Artificial Sequence: Primer

Query Match
? Best Local Similarity 15.7% Score 14.6; DB 4; Length 38;
? Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

? 4 CTGGGACGACCTCATCTGCTCC 24
? 17 | | | | | | | | | | | | | | | | | |
? Db 17 GAGCGACCCGCTCCGCGGTCAAGT 37

RESULT 39
? US-08-431-080-9
? Sequence 39: Application US/08431080
? Patent No. 569806
? GENERAL INFORMATION:
? APPLICANT: Singer, William S.
? INVENTOR: Singer, William S.
? TITLE OF INVENTION: Increase Compositions and Methods
? CORRESPONDENCE ADDRESS:
? STREET: P. O. BOX 14193
? CITY: HOUSTON
? STATE: TEXAS
? COUNTRY: UNITED STATES OF AMERICA
? ZIP: 77210
? COMPUTER READABLE FORM: disk
? MEDIUM TYPE: FLOPPY disk
? OPERATING SYSTEM: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII

? INFORMATION FOR SEQ ID NO: 9:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 35 base pairs
? TYPE: DNA
? STRANDEDNESS: double
? TOPOLOGY: linear
? Molecule type: DNA (genomic)

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? SOFTWARE: Patella Release #1.0, Version #1.30
? COUNTRY: UNITED STATES OF AMERICA
? APPLICATION NUMBER: US/08/431,080
? FILING DATE: Concurrently Here-with
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: SN 08/236,781
? CLASSIFICATION: October 20, 1994
? ATTORNEY/AGENT INFORMATION:
? NAME: RAYNE, David L.
? REFERENCE/COCKET NUMBER: 1,155
? TELECOMMUNICATION INFORMATION:
? TELEFAX: 713/789-5670
? TRIAX: 79-0924
? INFORMATION FOR SEQ ID NO: 9:
? SEQUENCE 39: Application US/08431080
? LENGTH: 40 base pairs
? TYPE: nucleic acid
? TOPOLOGY: linear
? US-08-431-080-9

Query Match
? Best Local Similarity 15.7% Score 14.6; DB 1; Length 40;
? Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

? 6 GAGCTGTGCGCTCCGCGGTCAAGT 34
? 1 | | | | | | | | | | | | | | | | | |
? Db 6 GAGCTGTGCGCTCCGCGGTCAAGT 34

RESULT 60
? US-08-185-9498-93C
? Sequence 59: Application US/08185949B
? Patent No. 587479
? GENERAL INFORMATION:
? APPLICANT: Mark D. Cochran
? INVENTOR: Richard D. McDonald
? TITLE OF INVENTION: Ribonucleic Acids
? NUMBER OF SEQUENCES: 104
? CORRESPONDENCE ADDRESS:
? STREET: 1185 Avenue of the Americas
? CITY: NEW YORK
? COUNTRY: USA
? ZIP: 10016
? COMPUTER: IBM 330 166 DXZ
? OPERATING SYSTEM: PC-DOS/MS-DOS
? OPERATING SYSTEM: IBM PC compatible
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/185,949B
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? REGISTRATION NUMBER: 678
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (212) 278-0400
? INFORMATION FOR SEQ ID NO: 99:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 35 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? Molecule type: DNA (genomic)

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Sun Jul 6 13:51:01 2003

US-09-843-377-3_1000_1092_621m50_7m1

Page 30

APPLICANT: NO
APPLICANT: NO
US-08-185-9198-99
Query Match 15 74; Score 14.6; DB 2; Length 40;
Best Local Similarity 69.04; Pred. No. 4, 9+03;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
OR 33 AATCGCTGCTTCACACATTCGCAAG 61
DB 39 AATGCTATATTTACATATCGGATG 11

RESULT 61
US-08-185-9198-99
Sequence 9; Application US/0893934
Patent No. 5161579
ORIGIN: UNKNOWN
APPLICANT: GONTSCHALL, Daniel E.
APPLICANT: Singer, William S.
TITLE OF INVENTION: Tetranucleotide Compositions and Methods
NUMBER OF SEQUENCES: 114
ADDRESSER: Arnold, White & Durkee
CORRESPONDENCE ADDRESS:
CITY: Houston
STATE: TEXAS
PRIORITY DATES AND STATES OF AMERICA
PRIORITY NUMBER: 08/931,080
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patent Release #1.0, Version #1.30
INFORMATION CHARACTERISTICS:
LENGTH: 40 bases
STANDARDS: single
TOPOLOGY: linear
US-08-938-534-9
Query Match 15 74; Score 14.6; DB 2; Length 40;
Best Local Similarity 59.74; Pred. No. 0+03;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
OR 63 GATCTGCGGCGCCGAAACATGATG 91
DB 6 GATCTGCTGCTTCACATTCGCAAG 34

RESULT 62
US-08-778-4848-100/C
Sequence 100; Application US/087784948
Matches 23; Conservative 0; Mismatches 0;
GENERAL INFORMATION:

APPLICANT: Chemchik, Alex
APPLICANT: Zhu, York
APPLICANT: Diachenko, Luda
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PVLV-LENGTH CNA
NUMBER OF SEQUENCES: 114
ADDRESSER: Salimovich, Lloyd & Salimovich
STREET: 4421 N.W. 41st Street, Suite A-1
CITY: Fort Lauderdale
STATE: Florida
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patent Release #1.0, Version #1.30
INFORMATION CHARACTERISTICS:
LENGTH: 40 bases
STANDARDS: single
TOPOLOGY: linear
US-08-778-4848-100
Query Match 15 74; Score 14.6; DB 2; Length 40;
Best Local Similarity 69.04; Pred. No. 4, 9+03;
Matches 23; Conservative 0; Mismatches 0;
OR 37 GCGCGCTGCGGCGCCGAAACATGCT 39
DB 37 GCGCGCTGCGGCGCCGAAACATGCT 1

RESULT 63
US-08-483-511-80
Sequence 80; Application US/08483511
Patent No. 6297148
ORIGIN: UNKNOWN
APPLICANT: O'Leary, Douglas F.
APPLICANT: O'Leary, William M.
APPLICANT: Lee, William T.L.
TITLE OF INVENTION: HEPATITIS THERAPEUTICS
NUMBER OF SEQUENCES: 84
ADDRESSER: O'Leary, Douglas F.
STREET: 6100 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: U.S.
ZIP: 98104
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible

APPLICANT: Valitex, Geneva
APPLICANT TYPE: Chemical/Laboratory Inc.
TITLE OR INVENTION: Chemtec Polydonal Antibodies
FILE REFERENCE: 014907-0070080
CURRENT FILING DATE: 1999-10-02/09/10/1903
PRIOR APPLICATION NUMBER: US 08/932,985
PRIOR FILING DATE: 1997-06-04/US 08/935,139
PRIOR PUBLICATION DATE: 1997-04-04
PRIOR APPLICATION NUMBER: 08/937,058/06/0704
NUMBER OF SEQ ID NOS: 100
SOFTWARE: FastSeq for Windows Version 3.0
SEQUENCE LENGTH: 43
TYPE: DNA
FEATURES:
OTHER INFORMATION: oligo 35
US-09-410-903-55
Query Match 15.7% Score 14.6; DB 4; Length 43;
Heat-Low Similarity 62.7%; Pred. No. 5.1e+03;
Matches 37 Conservative 0; Mismatches 14; Indels
QY 37 CCGTGGTTGTGACAGATGCAGATGTCAGCTGGAC 13
DB 39 CGCATGTTGACATGATGCAATCCGATCGAGTGCGTGGC 3

PRIEST 47
US-08-328-219-V/C
Sequence 4, Application US/0829379
PENDING INFORMATION:
REMARKS:
APPLICANT: Pfister, Catherine A.
INVENTOR: Pfister, Catherine A.
APPLICANT TYPE: Chem/Lab
APPLICANT: Van Cleve, Mark
INVENTOR: Wright, David J
TITLE OF INVENTION: THERMOHILIC ENZYMES
NUMBER OF SEQUENCES: 19
ADDRESS: ADDRESS 3
CORRESPONDING ADDRESS: 3
ADDRESSEE: Company
STREET: 1 Beeton Drive
STATE: NJ
COUNTRY: US
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPILER: IBM PC compatible
OPERATING SYSTEM: DOS
SOFTWARE: PicEdit Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 03/06/209, 219
CLASSIFICATION: 433
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: N 32,135
REFERENCE/DOCKET NUMBER: P 2961
INSTRUMENT CHARACTERISTICS: 4
LENGTH: 45 base pairs
TYPE: nucleic acid
SUBJECT: thermophilic enzyme
TOPOLGY: Linear
MOLECULE TYPE: DNA (genomic)

[illegible]

[illegible]

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1 TELEPHONE: (202) 408-4600
2
3 INFORMATION: (202) 408-4400
4
5 SOURCE CHARACTERISTICS:
6
7   LENGTH: 14 base pairs
8
9   STRANDNESS: 24964
10
11   TOPOLOGY: linear
12
13   SOURCE DESCRIPTION: (SRA)
14
15   SOURCE DESCRIPTION: SRA ID NO: 10:
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17 Query Match
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19   Matches 18: Conservative 9: Mismatches 6: Indels 0: Gaps 0
20
21   Best Local Similarity 75.0% Pct. No. 5.5e04
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23 GCCTGTTGATCGATCGCA 59
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25 GCCTGTTGATCGATCGCA 29
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DB 39 TCGGAGCTCCAGACCTCTCTGAG 16

RESULT 85
US-08-301-72A-6/C
Sequence 6, Application US/0810172A
GENERAL INFORMATION:
APPLICANT: Dhl, George R.
APPLICANT: Naderberg, David
APPLICANT: Naderberg, David
TITLE OF INVENTION: SOURCE OF HUMAN DOMINANT TRANSFEREE
TITLE OF INVENTION: CONA
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolsch & Birch, LLP
CITY: St. Louis
STATE: Virginia
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: COMPATIBLE
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 07-SEP-1994
CLASSIFICATION: 415.TOW.
NAME: Murphy, J.F., Gerald M.
REGISTRATION NUMBER: 28,977
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8000
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS: 6:
LENGTH: 40 base pairs
STRANDEDNESS: double
TOPOLOGY: linear
MUTATION: none
HYDROTHERMAL: ES
ANTI-SENSE: NO
FEATURE:
LOCATION: 1..40
OTHER INFORMATION: /label=consensus
OTHER INFORMATION: /index=consensus
OTHER INFORMATION: /untranslated=region of HIGH CONC
Query Match 15.5% Score 14.4; DB 3; Length 40;
Best Local Similarity 75.0%; Pred. No 6e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

CORRESPONDENCE ADDRESS:

ADDRESSEE: Birch, Stewart, Kolsch & Birch, P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

COUNTRY: US

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: IBM Compatible

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/597,559

CLASSIFICATION: No. 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/01467

REFERENCE/DOCCT NUMBER: 31,238

NAME: Lash, John M.

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-678-1069

TELEFAX: 619-678-1069

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 48

STRANDEDNESS: single

TOPOLOGY: linear

MUTATION TYPE: genomic DNA

US-08-687-559-19

Query Match 15.5% Score 14.4; DB 2; Length 44;

Best Local Similarity 75.0%; Pred. No. 6.2e+03;

Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

DB 37 TCGAGCTCCAGACCTCTCTGAG 21

RESULT 87
US-08-145-704-44
Sequence 44, Application US/08145704
GENERAL INFORMATION:
APPLICANT: Bando, Robert F.
APPLICANT: Penwald, Susan G.
APPLICANT: Josenberg, Joseph G.
TITLE OF INVENTION: Anti-Viral Gaussoins-Rich
TITLE OF INVENTION: Oligonucleotides
CORRESPONDENCE ADDRESS:
ADDRESSEE: Phil Light, & Jinczak
CITY: Houston
STATE: Texas
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 28-OCT-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:

1 SEQUENCE 40
 2 US-09-017-974-44
 3 / Sequence 44, Application US/09011974
 4 / Patent No. 6388044
 5 / GENERAL INFORMATION:
 6 APPLICANT: Ando, Robert F.
 7 APPLICANT: Ojwang, Joshua O.
 8 APPLICANT: Bogdan, Michael E.
 9 APPLICANT: Zendejuli, Joseph G.
 10 APPLICANT: Cosman, Paul A.
 11 APPLICANT: Cosman, Paul A.
 12 TITLE OF INVENTION: Anti-viral Guanosine-Rich
 13 NUMBER OF SEQUENCES: 89
 14 CORRESPONDENCE ADDRESS:
 15 STREET: 600 Congress, Suite 4, Teyon, P.C.
 16 CITY: Houston
 17 COUNTRY: Texas
 18 STATE: Texas
 19 ZIP: 77002-2912
 20 COMPUTER READABLE FORM:
 21 OPERATING SYSTEM: IBM PC compatible
 22 OPERATING SYSTEM: PC-DOS/MS-DOS
 23 OPERATING SYSTEM: MS Word 97 (saved as .txt file)
 24 CURREN APPLICATION DATA:
 25 APPLICATION NUMBER: US/09/017-974
 26 FILING DATE:
 27 PRIORITY INFORMATION:
 28 PRIORITY INFORMATION:
 29 APPLICATION NUMBER: 60/097,374
 30 APPLICATION NUMBER: 97
 31 FILING DATE: 09-DEC-97
 32 ATTORNEY/AGENT INFORMATION:
 33 REFERENCE/DOCKET NUMBER: 33-962
 34 REGISTRATION NUMBER: 1472-06223
 35 TELEPHONE: 713/238-8010
 36 TELEFAX: 713/238-8008
 37 INVENTION FOR SEQ ID NO: 44:
 38 SEQUENCE CHARACTERISTICS:
 39 LENGTH: 47 base pairs
 40 TYPE: nucleic acid
 41 TOPOLOGY: linear
 42 MOLECULE TYPE: DNA (genomic)
 43 US-09-017-974-44
 44 Query Match 15.5% Score 14.4; DN 4; Length 47;
 45 Best Local Similarity 65.6%; Pred. No. 6.4e+03;
 46 Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
 47 DB 6 TTTCGACCTTCGATCGATGATCTCGGCC 74

1 TITLE OF INVENTION: Anti-viral Guanosine-Rich
 2 NUMBER OF SEQUENCES: 87
 3 CORRESPONDENCE ADDRESS:
 4 STREET: 600 Congress, Suite 4, Teyon, P.C.
 5 CITY: Houston
 6 COUNTRY: U.S.A.
 7 STATE: Texas
 8 ZIP: 77002-2912
 9 COMPUTER READABLE FORM:
 10 OPERATING SYSTEM: IBM PC compatible
 11 OPERATING SYSTEM: MS Windows 95
 12 OPERATING SYSTEM: MS Word 97 (saved as .txt file)
 13 CURREN APPLICATION DATA:
 14 APPLICATION NUMBER: US/08/582,255A
 15 FILING DATE: 03-APR-96
 16 PRIORITY INFORMATION:
 17 PRIORITY INFORMATION:
 18 APPLICATION NUMBER: US 08/335,168
 19 APPLICATION NUMBER: 60/001,505
 20 FILING DATE: 15-JULY-95
 21 FILING DATE: 25-MARCH-96
 22 APPLICATION NUMBER: 60/013,688
 23 APPLICATION NUMBER: 60/019,714
 24 FILING DATE: 17-APRIL-96
 25 APPLICATION NUMBER: 60/016,271
 26 PRIORITY INFORMATION:
 27 ATTORNEY/AGENT INFORMATION:
 28 NAME: McDaniel, C. Steven
 29 REFERENCE/DOCKET NUMBER: 33-962
 30 REGISTRATION NUMBER: 1472-06214
 31 TELEPHONE: 713/238-8010
 32 INVENTION FOR SEQ ID NO: 44:
 33 SEQUENCE CHARACTERISTICS:
 34 LENGTH: 47 base pairs
 35 TYPE: nucleic acid
 36 TOPOLOGY: linear
 37 MOLECULE TYPE: DNA (genomic)
 38 US-08-682-255A-44
 39 Query Match 15.5% Score 14.4; DN 4; Length 47;
 40 Best Local Similarity 65.6%; Pred. No. 6.4e+03;
 41 Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
 42 DB 6 TTTCGACCTTCGATCGATGATCTCGGCC 74

1 SEQUENCE 32
 2 US-08-682-255A-44
 3 / Sequence 44, Application US/08682255A
 4 / Patent No. 635785
 5 / GENERAL INFORMATION:
 6 APPLICANT: Ando, Robert F.
 7 APPLICANT: Ojwang, Joshua O.
 8 APPLICANT: Bogdan, Michael E.
 9 APPLICANT: Zendejuli, Joseph G.
 10 APPLICANT: Cosman, Paul A.
 11 APPLICANT: Cosman, Paul A.
 12 TITLE OF INVENTION: Anti-viral Guanosine-Rich
 13 NUMBER OF SEQUENCES: 89

1 SEQUENCE 32
 2 US-08-682-255A-44
 3 / Sequence 44, Application US/09429130
 4 / Patent No. 635785
 5 / GENERAL INFORMATION:
 6 APPLICANT: Ando, Robert F.
 7 APPLICANT: Ojwang, Joshua O.
 8 APPLICANT: Bogdan, Michael E.
 9 APPLICANT: Zendejuli, Joseph G.
 10 APPLICANT: Cosman, Paul A.
 11 APPLICANT: Cosman, Paul A.
 12 TITLE OF INVENTION: Anti-viral Guanosine-Rich
 13 NUMBER OF SEQUENCES: 89

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Conley, Rose & Tayon, P.C.
 STREET: 600 Travis, Suite 1850
 CITY: Houston
 STATE: TEXAS
 COUNTRY: U.S.A.
 ZIP: 77002-2912
 COMPUTER READABLE FORM:
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: MS Word 97 (saved as .txt file)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/429,130
 CLASSIFICATION: 19-JULY-95
 PRIORITY NUMBER: 19-MARCH-96
 FILING DATE: 17-APRIL-96
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/682,255
 FILING DATE: KINSHAWD
 FILING DATE: 19-JULY-95
 APPLICATION NUMBER: 6/014,007
 FILING DATE: 19-JULY-95
 APPLICATION NUMBER: 6/013,688
 FILING DATE: 15-MARCH-96
 FILING DATE: 17-APRIL-96
 ATTORNEY/AGENT INFORMATION:
 NAME: MICHAEL, C. STEVEN
 REGISTRATION NUMBER: 33,962
 TELECOMMUNICATION INFORMATION:
 REFERENCE/DOCKET NUMBER: 1472-06214
 TELEPHONE: 713/238-8008
 INFORMATION FOR SEQ ID NO: 44:
 SEQID: 47 base pairs
 LENGTH: 47 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 MOLECULE TYPE: DNA (genomic)
 SEQUENCE DESCRIPTION: SEQ ID NO: 44:
 US-09-429-130-44
 Query Match Best Local Similarity 13.5% Score 14.4; DB 4; Length 47;
 Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
 43 TTTCACACATGCGATGATGATCGTCGCGCC 74
 6 TTGGCAACCTTGGAACCTGACCTGACCTGCGCC 37
 RESULT 93
 PCT-US96-11786-44
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Conley, Rose & Tayon, P.C.
 STREET: 600 Travis, Suite 1850
 CITY: Houston
 STATE: TEXAS
 COUNTRY: U.S.A.
 ZIP: 77002-2912
 COMPUTER READABLE FORM:
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: MS Word 97 (saved as .txt file)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/429,130
 CLASSIFICATION: 19-JULY-95
 PRIORITY NUMBER: 19-MARCH-96
 FILING DATE: 17-APRIL-96
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/682,255
 FILING DATE: KINSHAWD
 FILING DATE: 19-JULY-95
 APPLICATION NUMBER: 6/014,007
 FILING DATE: 19-JULY-95
 APPLICATION NUMBER: 6/013,688
 FILING DATE: 15-MARCH-96
 FILING DATE: 17-APRIL-96
 ATTORNEY/AGENT INFORMATION:
 NAME: MICHAEL, C. STEVEN
 REGISTRATION NUMBER: 33,962
 TELECOMMUNICATION INFORMATION:
 REFERENCE/DOCKET NUMBER: 1472-06214
 TELEPHONE: 713/238-8008
 INFORMATION FOR SEQ ID NO: 44:
 SEQID: 47 base pairs
 LENGTH: 47 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 MOLECULE TYPE: DNA (genomic)
 SEQUENCE DESCRIPTION: SEQ ID NO: 44:
 US-09-429-130-44

ADDRESSEE: Conley, Rose & Tayon, P.C.
 STREET: 600 Travis, Suite 1850
 CITY: Houston
 STATE: TEXAS
 COUNTRY: U.S.A.
 ZIP: 77002-2912
 COMPUTER READABLE FORM:
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: MS Word 97 (saved as .txt file)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/11786
 CLASSIFICATION: 19-JULY-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/735,168; 6/001,505; 6/014,007; 6/013,688;
 APPLICATION NUMBER: 6/013,688
 FILING DATE: 23-OCT-95; 17-JULY-96; 23-MARCH-96; 19-MARCH-96; 23-
 FILING DATE: APRIL-96; 17-APRIL-96
 NAME: MICHAEL, C. STEVEN
 REGISTRATION NUMBER: 33,962
 TELECOMMUNICATION INFORMATION:
 REFERENCE/DOCKET NUMBER: 1472-06214
 TELEPHONE: 713/238-8008
 INFORMATION FOR SEQ ID NO: 44:
 SEQID: 47 base pairs
 LENGTH: 47 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 MOLECULE TYPE: linear
 PCT-US96-11786-44
 Query Match Best Local Similarity 13.5% Score 14.4; DB 3; Length 47;
 Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
 43 TTTCACACATGCGATGATGATCGTCGCGCC 74
 6 TTGGCAACCTTGGAACCTGACCTGACCTGCGCC 37
 RESULT 94
 US-09-916-5768-26/C
 Patent No. 6,718,165
 GENERAL INFORMATION:
 APPLICANT: VILLOD, PATRICK J.
 APPLICANT: BERNER, BERNARD
 APPLICANT: BERNER, GREGORY A.
 NUMBER OF SEQUENCES: 43
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GUSTAFSON & FOX, P.L.L.C.
 STREET: 1100 NEW YORK AVENUE, SUITE 100
 CITY: WASHINGTON
 STATE: DC
 ZIP: 20005-9924
 COMPUTER READABLE FORM:
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: MS Word 97 (saved as .txt file)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/716,5768
 FILING DATE: 19-MARCH-96
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 06/024,347
 FILING DATE: 23-06-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: STEVE ERIC K.
 REFERENCE/DOCKET NUMBER: 1488 0500001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 2021 311-1111
 TELEFAX: 2021 311-1111
 INFORMATION FOR SEQ ID NO: 26:
 SOURCE CHARACTERISTICS:
 ORGANISM: HUMAN
 TYPE: nucleic acid
 STRANDNESS: single
 MOLECULE TYPE: cDNA
 US-06-516-5768-26
 Query Match 15.5%; Score 14.4; DB 4; Length 49;
 Best Local Similarity 60.0%; Pred. No. 6.6e+03;
 Matches 24; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
 Oy 53 ATCGAATGTCAGTCGCGCCGCGGAAACATGTAAGT 92
 Db 41 ATGAAATGTCCTCTTTCATCGAGAGAGCTGCGCT 2

RESUME 95
 US-09-049-475-7
 Sequence No. 7; Application US/0904975
 Patent No. 6140354
 OTHER INFORMATION:
 APPLICANT: O'Reilly, David
 APPLICANT: Thomas, Christopher
 APPLICANT: O'Reilly, David
 TITLE OF INVENTION: SPECIFICITY OF GENE EXPRESSION
 NUMBER OF SEQUENCES: 7
 ADDRESS: 1155 Avenue of the Americas
 CITY: New York
 COUNTRY: USA
 ZIP: 10036-2711 USA
 COMPLETION DATE: 1997
 MEDICAL TYPE: Diagnostic
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: PASTELIN BALANCE 81.0, Version #1.30
 CURRENT APPLICATION DATA: Application 2.0
 APPLICATION NUMBER: US/09/049,475
 CLASSIFICATION: 800 1599
 PRIOR APPLICATION DATA: 9706381.2
 FILING DATE: 16-NOV-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: COZZIEL, LAURE A
 REFERENCE/DOCKET NUMBER: 9341-014-999
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 2121669910
 TELEFAX: 2121669910
 TEXT: 66141 PNNIE 7:
 INFORMATION FOR SEQ ID NO: 7:
 SOURCE CHARACTERISTICS:
 ORGANISM: HUMAN
 TYPE: nucleic acid
 STRANDNESS: single
 LENGTH: 20 base pairs
 TOPOLOGY: linear
 MOLECULE TYPE: other
 ORIGINAL SOURCE

RESUME 96
 US-08-513-9748-81/C
 Sequence No. 6; Application US/085139748
 Patent No. 6140354
 OTHER INFORMATION:
 APPLICANT: Huma, Shaji
 APPLICANT: Huma, Shaji
 APPLICANT: Fujii, Iyo
 APPLICANT: Ohaki, Tetsuya
 APPLICANT: Ohai, Katsuhito
 TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
 NUMBER OF SEQUENCES: 180
 ADDRESS: 1155 Avenue of the Americas
 CITY: Boston
 COUNTRY: USA
 ZIP: 02109
 COMPLETION DATE: 1997
 MEDICAL TYPE: Diagnostic
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PASTELIN BALANCE 81.0, Version #1.30
 CURRENT APPLICATION DATA: Application 1.0
 APPLICATION NUMBER: US/08/513,9748
 FILING DATE: 14-SEP-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/JP95/01599
 FILING DATE: 10-AUG-1995
 APPLICATION NUMBER: JP 7-093989
 FILING DATE: 15-AUG-1995
 APPLICATION NUMBER: JP 7-057186
 FILING DATE: 16-NOV-1995
 APPLICATION NUMBER: JP 7-007177
 FILING DATE: 20-JAN-1995
 PRIOR APPLICATION DATA: JP 6-326611
 FILING DATE: 28-DEC-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-210017
 FILING DATE: 02-NOV-1994
 APPLICATION NUMBER: JP 6-263557
 FILING DATE: 30-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-263596
 APPLICATION NUMBER: JP 6-189274
 PRIOR APPLICATION DATA: 1994
 APPLICATION NUMBER: JP 6-189273
 FILING DATE: 11-AUG-1994
 PRIOR APPLICATION DATA:

RESUME 97
 US-09-049-475-7
 Sequence No. 7; Application US/0904975
 Patent No. 6140354
 OTHER INFORMATION:
 APPLICANT: O'Reilly, David
 APPLICANT: Thomas, Christopher
 APPLICANT: O'Reilly, David
 TITLE OF INVENTION: SPECIFICITY OF GENE EXPRESSION
 NUMBER OF SEQUENCES: 7
 ADDRESS: 1155 Avenue of the Americas
 CITY: New York
 COUNTRY: USA
 ZIP: 10036-2711 USA
 COMPLETION DATE: 1997
 MEDICAL TYPE: Diagnostic
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: PASTELIN BALANCE 81.0, Version #1.30
 CURRENT APPLICATION DATA: Application 2.0
 APPLICATION NUMBER: US/09/049,475
 CLASSIFICATION: 800 1599
 PRIOR APPLICATION DATA: 9706381.2
 FILING DATE: 16-NOV-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: COZZIEL, LAURE A
 REFERENCE/DOCKET NUMBER: 9341-014-999
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 2121669910
 TELEFAX: 2121669910
 TEXT: 66141 PNNIE 7:
 INFORMATION FOR SEQ ID NO: 7:
 SOURCE CHARACTERISTICS:
 ORGANISM: HUMAN
 TYPE: nucleic acid
 STRANDNESS: single
 LENGTH: 20 base pairs
 TOPOLOGY: linear
 MOLECULE TYPE: other
 ORIGINAL SOURCE

APPLICATION NUMBER: JP 6-189372
 FILING DATE: 11-AUG-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: [REDACTED]
 REGISTRATION NUMBER: 34,235
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INVENTOR: [REDACTED]
 SPOKESMAN: [REDACTED]
 LENGTH: 27 base pairs
 TYPE: nucleic acid
 STANDARDS: single
 MOLECULE TYPE: DNA
 US-08-310-011-16
 Query Match 15.3% Score 14.2; DB 3; Length 27;
 Best Local Similarity 84.2% Pred. No. 6.e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

DB 65 CTTGGGCGCTTCCTGAAA 83
 26 CTTGGGCGCTTCCTGAAA 8

RESULT 97
 US-08-340-011-16
 Sequence 16, Application US/08340011
 FILING DATE: 07-09-1994
 GENERAL INFORMATION:
 APPLICANT: ALLILLO, et al.
 TITLE OF INVENTION: P4, A NOVEL RECEPTOR TYROSIN KINASE
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS: C/O C/O J. Gertel, Murray & Brown
 STREET: 2300 South Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 OPERATING SYSTEM: PC-DOS/MS-DOS
 COMPILER: IBM PC COMPATIBLE
 CURRENT APPLICATION DATA: Release #1.0; Version #1.25
 APPLICATION NUMBER: US/08/340.011
 FILING DATE: 07-09-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/959,951
 ATTORNEY/AGENT INFORMATION:
 NAME: Weyers, Thomas C.
 REGISTRATION NUMBER: 36,989
 TELEPHONE: 312/474-6300
 TELEFAX: 312/474-0448
 TELECOMMUNICATION INFORMATION:
 INFORMATION FOR SEQ ID NO: 16:
 LENGTH: 28 base pairs
 TYPE: nucleic acid
 STANDARDS: single
 MOLECULE TYPE: DNA
 US-08-340-011-16
 Query Match 15.3% Score 14.2; DB 1; Length 28;
 Best Local Similarity 84.2% Pred. No. 6.1e+03;
 Matches 16;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 DB 65 GGGAGCATGCTATCTGCC 24
 2 GGGAGCATGCTATCTGCC 20

RESULT 98
 US-08-901-710-16
 Sequence 16, Application US/08901710
 FILING DATE: 07-09-1994
 GENERAL INFORMATION:
 APPLICANT: ALLILLO, Karl
 TITLE OF INVENTION: P4, A RECEPTOR TYROSINE KINASE, AND USES
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 STREET: 2300 South Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 OPERATING SYSTEM: PC-DOS/MS-DOS
 COMPILER: IBM PC COMPATIBLE
 CURRENT APPLICATION DATA: Release #1.0; Version #1.25
 APPLICATION NUMBER: US/08/901.710
 FILING DATE: 07-09-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/340.011
 PRIOR APPLICATION DATA: 1994
 APPLICATION NUMBER: 08/757,754
 PRIOR APPLICATION DATA: 1994
 APPLICATION NUMBER: 07/959,951
 FILING DATE: 07-09-1994
 NAME: Gertel, Murray & Brown
 REGISTRATION NUMBER: 36,153
 TELEPHONE: 312/474-6300
 TELEFAX: 312/474-0448
 TELECOMMUNICATION INFORMATION:
 INFORMATION FOR SEQ ID NO: 16:
 LENGTH: 28 base pairs
 TYPE: nucleic acid
 STANDARDS: single
 MOLECULE TYPE: DNA
 US-08-901-710-16
 Query Match 15.3% Score 14.2; DB 3; Length 28;
 Best Local Similarity 84.2% Pred. No. 6.1e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

DB 6 GGGAGCATGCTATCTGCC 24
 2 GGGAGCATGCTATCTGCC 20

```

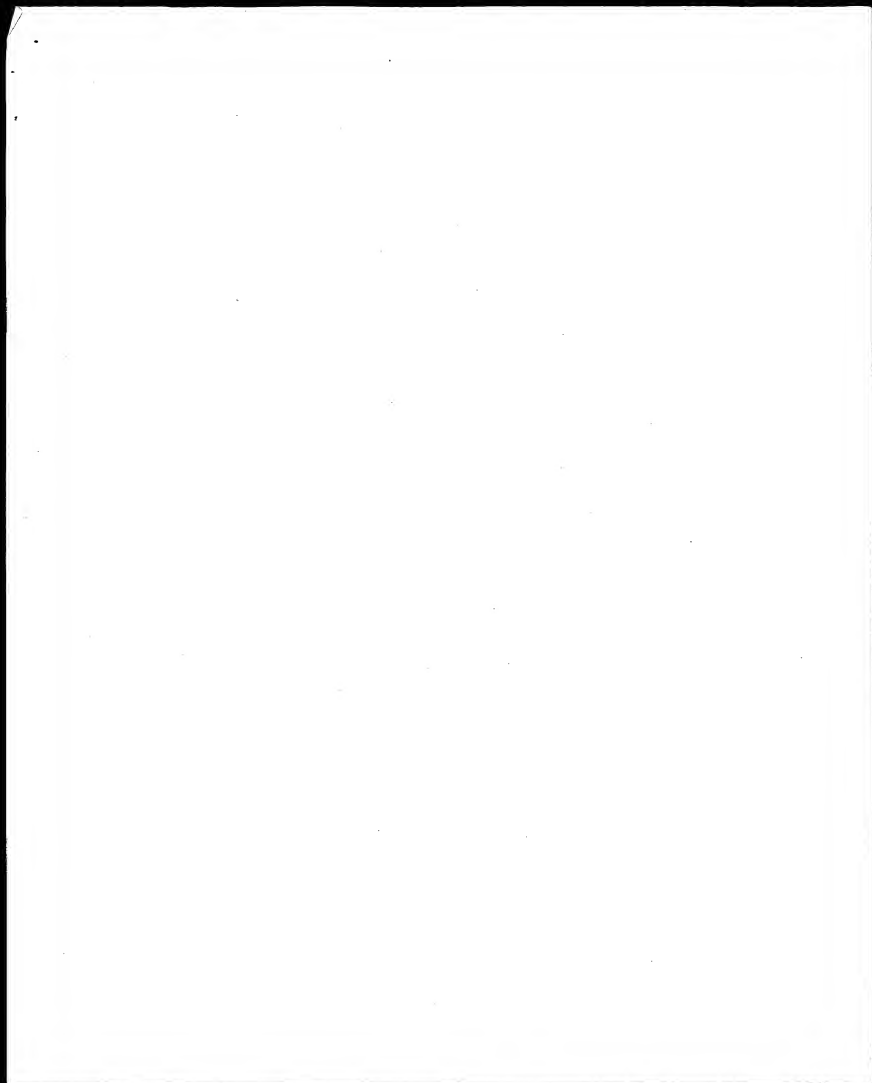
RESULT 99
US-08-331-081B-16/c
Sequence 16, Application US/08/331081B
PARENTAL: 3596970
APPLICANT: McMillin, Robert H.
TITLE OF INVENTION: Transgenic Fish and Vectors Therefor
CORRESPONDENCE ADDRESS:
ADDRESSER: McRadden, Fisham
CITY: 233 McMillin Street, Suite 606
STATE: Ontario
COUNTRY: Canada
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch, 1.44 MD
COMPILED: IBM PC or Compatible
OPERATING SYSTEM: PC DOS 5.0
CHECKED APPLICATION: 5.1 (Patseq.txt)
APPLICATION NUMBER: US/08/331,081B
FILING DATE: October 20, 1994
PRIORITY DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: Canada 2,126,138
ATTORNEY/AGENT INFORMATION:
NAME: Fisham, H. Ian
REGISTRATION NUMBER: 67,375
TELEPHONE: (613) 234-1507
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
TYPE: Nucleic acid
STRANDNESS: single (part of double)
US-08-331-081B-16
Query Match 15.3%, Score 14.2, DB 2, Length 29,
Best local similarity 70.4%, Pred. No 6.3e+03
Matches 19, Conservative 0, Mismatches 8, Indels 0, Gaps 0,
Or 17 CCGTGGCGGCGACGACGACGCGTGGT 43
Db 28 ATTCCGCCCGGCGGCGACGCGTGGAN 2
RESULT 100
US-08-627-907A-8
Sequence 8, Application US/08/627907A
Patent No. 6060102
GENERAL INFORMATION:
APPLICANT: BILLY H. HENDRI
TITLE OF INVENTION: HUMAN PROSMOLIPASE C-ALPHA AND DNA
CORRESPONDENCE ADDRESS:
ADDRESSER: C/O FISH & MEYER
CITY: New York
STATE: New York
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

```

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SOFTWARE: Patent release #1.0, Version #1.30
COUNTRY: Canada
APPLICATION NUMBER: US/08/627 907A
FILING DATE:
PRIORITY DATE: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 5 238402
FILING DATE: 21-SEP-1993
PRIORITY DATE: 27-SEP-1994
FILING DATE: 27-SEP-1994
PRIORITY DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/01572
NAME: BALEY JR, James F.
REGISTRATION NUMBER: 27,794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9090
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
STRANDNESS: single
TOPOLGY: linear
DESCRIPTION: other nucleic acid
US-08-627-907A-8
Query Match 15.3%, Score 14.2, DB 3, Length 30,
Best local similarity 70.4%, Pred. No 6.3e+03
Matches 19, Conservative 0, Mismatches 8, Indels 0, Gaps 0,
Or 37 CCGTGGCGGCGACGACGACGCGTGGT 63
Db 4 CCGTGGCGGCGACGACGACGCGTGG 10
Search completed: July 5, 2003, 13:10:03
500 time : 69 secs

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GenCore version 5.1.6
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OK nucleic - nucleic search, using sw model

Run on: July 5, 2003 10:01:04 Search time 1157 seconds

(without alignments)
1109,934 Million cells updates/sec

Title: US-09-843-377-3_COPY_1000_1092

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Scoring table: IDENTITY, NUC

Group 10.0, Offset 1.0

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Listing files: 1000 summaries

Database: EST

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27: em.estbta.*

Prod. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Query	Match length	DB ID	Description
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2	18.2	19.6	47	17	AL78166
3	17.6	18.9	50	9	AL78166
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[illegible]

RESULT 18
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 VERSION BR555656.1 GI:3803415
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 ORGANISM Homo sapiens
 FEATURES
 SOURCE
 REFERENCE
 AUTHORS NIH-MGC
 JOURNAL Unpublished (1999)
 COMMENT
 Tissue: spleen
 Contact: Robert Strimberg, Ph.D.
 cDNA Library Prepared by: The I.M.A.G.E. Consortium (ILM)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILM)
 Clone Distribution: I.M.G.E. Clone distribution information can be found through the I.M.A.G.E. Consortium/ILM at: imgc.llnl.gov
 High quality sequence: 49
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 /db_xref="taxon:9606"
 /clone="ILM-MGC_8"
 /library_type="Bacterial lymphoma"
 /note="cDNA (phage resistant)"
 /note="cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XbaI sites using the following 5' insert size 1.8kb. Library constructed by cloning in the laboratory of Gerald M. Rubin (University of Strasbourg and Supagene) using 1P (full term) synthesis."

QUERY MATCH 16.6% Score 15.4; DB 10; Length 49;
 Match Local Similarity 61.0%; Pred. No. 2.7e-05;
 Matches 25; Conserved sites 0; Mismatches 16; Indels 0; Gaps 0;
 DB 17 ATTCTCCCTGGTGGTCAACAGCTGGTTCACACATCGG 57
 DB 3 ACTTGGCTGGTGGTCAACAGCTGGTTCACACATCGG 43

RESULT 19
 JOURNAL
 DEFINITION 50 bp mRNA linear EST 30-AUG-2001
 ACCESSION
 VERSION AU066333.1 GI:13555854
 SOURCE
 ORGANISM human
 FEATURES
 SOURCE
 REFERENCE
 AUTHORS Suzuki, T., Tanaka, T., Morishita, S., Oshio, Y., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

TITLE
 JOURNAL
 DEFINITION 21270072 Yuxaka Shunko
 ACCESSION
 VERSION 21270072
 SOURCE
 ORGANISM Yuxaka Shunko
 FEATURES
 SOURCE
 REFERENCE
 AUTHORS Department of Virology
 Institute of Medical Science, University of Tokyo
 Email: yusaka@ims.s.u-tokyo.ac.jp
 Suzuki, Y., Yoshitomo Nakagawa, K., Miyagawa, K., Suyama, A. and Sugano, S.
 Construction and characterization of a full length-enriched and 5' end-enriched cDNA library. Genes 200 (1-2), 149-156 (1997).
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="ILM-MGC_8"
 /note="Differential display competition of untreated and dimethylsulfoxide treated U937 cells"

QUERY MATCH 16.6% Score 15.4; DB 9; Length 50;
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 Matches 25; Conserved sites 0; Mismatches 16; Indels 0; Gaps 0;
 DB 10 GATCTCCCTGGTGGTCAACAGCTGGTTCACACATCGG 50
 DB 44 GATCTCCCTGGTGGTCAACAGCTGGTTCACACATCGG 44

RESULT 20
 JOURNAL
 DEFINITION 50 bp mRNA linear EST 30-AUG-2001
 ACCESSION
 VERSION AU066333.1 GI:13555854
 SOURCE
 ORGANISM human
 FEATURES
 SOURCE
 REFERENCE
 AUTHORS Suzuki, T., Tanaka, T., Morishita, S., Oshio, Y., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

QUERY MATCH 16.6% Score 15.4; DB 9; Length 50;
 Match Local Similarity 61.0%; Pred. No. 2.7e-05;
 Matches 25; Conserved sites 0; Mismatches 16; Indels 0; Gaps 0;
 DB 10 GATCTCCCTGGTGGTCAACAGCTGGTTCACACATCGG 50
 DB 44 GATCTCCCTGGTGGTCAACAGCTGGTTCACACATCGG 44


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/db_xref="taxon:9606"
/clone="IMAGE150518"
/contig="150518"
/seq="seq_N7L1_ORF_S1"
/seq_host="brihs"
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a modified polylinker; Site.1: Not.1; Site.2: Eco RI;
Site.3: Not.1; Site.4: Not.1; Site.5: Not.1; Site.6:
Not.1; Site.7: Not.1; Site.8: Not.1; Site.9: Not.1;
NCI(GAP-GS1) were mixed; and as circles were made in
the presence of 100 ng/ml of the same restriction enzyme
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
1000 clones each. The pools were then amplified by
72608-72811, and 72996-73199. Subtraction by Benzo
Soares and M. Filina Bonaldi.

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BASE COUNT

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12 a
14 c
14 g
19 t

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ORIGIN

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Query Match      14 88      Score 13.8      DB 9; Length 49;
Best Local Similarity 63.8%; Pctid 10.4e+00; 12; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 88
56 GGAATGCTGACTGCGCGCTGCTGCAAACTTGTG 88
OR      |||||      |||||      |||||      |||||
DB      33 GGATTAACCTGTGTGCTCCGAAAGAGTTG 1

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Search completed: July 5, 2003, 13:09:21
 Job time : 1409 secs

